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OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 09:15:47 ; Search time 7739.27 Seconds  
(without alignments)  
11105.593 Million cell updates/sec

Title: US-10-001-227-1  
Perfect score: 1983  
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Scoring table: IDENTITY NUC  
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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

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and is derived by analysis of the total score distribution.

SUMMARIES

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1	1983	100.0	1983	6	AX469746 Sequence
2	1928.6	97.3	2081	6	AX377796 Sequence
3	1752	88.4	1752	6	AX469748 Sequence
4	1459.4	73.6	2178	6	AX833215 Sequence
5	1459.4	73.6	2178	9	AK094783 Homo sapi
6	1073.2	54.1	2448	10	BC026374 Mus muscu
7	1013	51.1	2456	6	AX375990 Sequence
8	1013	51.1	2456	6	AX469751 Sequence
9	1013	51.1	2456	9	AX358504 Homo sapi
10	902	45.5	2178	6	AX377795 Sequence
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12	434.4	21.9	1985	4	AB094147 Felis cat
13	431.8	21.8	1923	4	AB023629 Canis fam
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18	426.2	21.5	1966	6	AX329628 Sequence
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25	417.4	21.0	1918	10	RATCHES
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34	412.6	20.8	2141	6	AX401835 Sequence
35	412.6	20.8	2141	10	RRESHVEL
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ALIGNMENTS

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DEFINITION Sequence 1 from Patent WO244357.  
ACCESSION AX469746  
VERSION AX469746.1 GI:21901868  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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Kapeller-Libermann, R. and Silos-Santiago, I.  
METHODS of using 18903 to treat pain and pain-related disorders  
Patent: WO 0244357-A 1 06-JUN-2002;  
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AUTHORS  
TITLE  
JOURNAL





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RESULT 2
AX377796
LOCUS AX377796 2081 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 29 from Patent WO0212467.
ACCESSION AX377796
VERSION AX377796.1 GI:19573887
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SOURCE Homo sapiens (human)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
1 Baughn, M.R., Bruns, C.M., Das, D., Deleage, A.M., Ding, L.,
  Elliot, V.S., Gandhi, A.R., Griffin, J.A., Hafalia, A.J., Khan, F.A.,
  Lal, P., Lee, S., Lu, D.A., Lu, Y., Patterson, C., Ramkumar, J.,
  Ring, H.Z., Sanjanwala, M.S., Tang, Y.T., Thornton, M. and
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VERSION AX833215.1 GI:39919350  
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Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahara, K. and

Masuko, Y.  
Full-length cDNA sequences  
Patent: EP 1347046-A 339 24-SEP-2003;  
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RESULT 9  
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LOCUS Homo sapiens clone DNA44179 carboxylesterase H1o (UNQ440) mRNA,  
complete cds.  
ACCESSION AY358504  
VERSION AY358504.1 GI:37182130  
KEYWORDS FLI\_CDNA.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2456)  
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,  
Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,  
Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,  
Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,  
Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieland,D., Woods,K.,  
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,  
Goddard,A., Wood,W.I. and Godowski,P.  
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale  
Effort to Identify Novel Human Secreted and Transmembrane Proteins:  
A Bioinformatics Assessment  
Genome Res. 13 (10), 2265-2270 (2003)  
JOURNAL 12975309  
PUBMED 2 (bases 1 to 2456)  
REFERENCE Clark,H.F.  
AUTHORS Direct Submission  
TITLE Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,  
JOURNAL Inc., 1 DNA Way, South San Francisco, CA 94080, USA  
FEATURES  
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ORIGIN  
Query Match 51.1%; Score 1013; DB 9; Length 2456;  
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RESULT 10  
 Locus AX377795  
 DEFINITION Sequence 28 from Patent WO0212467.  
 ACCESSION AX377795  
 VERSION AX377795.1 GI:19573886

KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 REFERENCE 1 Baughn, M.R., Bruns, C.M., Das, D., Deleage, A.M., Ding, L., Elliot, V.S., Gandhi, A.R., Griffin, J.A., Hafalia, A.J., Khan, F.A., Lai, P., Lee, S., Lu, D.A., Lu, X., Patterson, C., Rankumar, J., Ring, H.Z., Sanjanwalla, M.S., Tang, Y.T., Thornton, M. and Tribouley, C.M.  
 TITLE Drug metabolizing enzymes  
 JOURNAL Patent: WO 0212467-A 28 14-FEB-2002; Incyte Genomics, Inc. (US)  
 FEATURES  
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Query Match 45.5%; Score 902; DB 6; Length 2178;  
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 Matches 902; Conservative 0; Mismatches 0

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TITLE Molecular cloning of the feline liver carboxylesterase

JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 1985)  
 AUTHORS Miyazaki,M., Sai,H., Taira,H. and Yamashita,T.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-OCT-2002) Masao Miyazaki, Iwate University,  
 Department of Agro-bioscience, Faculty of Agriculture, 3-18-8 Ueda,  
 Morioka, Iwate 020-8550, Japan (E-mail:cdg83700@par.odn.ne.jp,  
 Tel:81-19-621-6157, Fax:81-19-621-6177)  
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source

gene  
 CDS

ORIGIN  
 Query Match 21.9%; Score 434.4; DB 4; Length 1985;  
 Best Local Similarity 57.1%; Pred. No. 4.2e-84;  
 Matches 855; Conservative 0; Mismatches 631; Indels 12; Gaps 3;

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RESULT 13  
 AB023629  
 LOCUS

1923 bp mRNA linear MAM 09-JUN-2001

DEFINITION Canis familiaris CESD1 mRNA for carboxylesterase D1, complete cds.

ACCESSION AB023629  
VERSION AB023629.1 GI:14331124  
KEYWORDS carboxylesterase D1; Dog liver carboxylesterase D1.  
SOURCE Canis familiaris (dog)

ORGANISM  
Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE  
1 (sites)  
Hosokawa, M., Suzuki, K., Takahashi, D., Mori, M., Satoh, T. and  
Chiba, K.

TITLE  
Purification, molecular cloning, and functional expression of dog  
liver microsomal acyl-CoA hydrolase: a member of the  
carboxylesterase multigene family

JOURNAL Arch. Biochem. Biophys. 389 (2), 245-253 (2001).  
MEDLINE 21237951  
PUBMED 11339814

REFERENCE  
2 (bases 1 to 1923)  
Hosokawa, M.

AUTHORS  
Direct Submission  
Submitted (11-FEB-1999) Masakiyo Hosokawa, Chiba University,  
Faculty of Pharmaceutical Sciences, 1-33 Yayoi-cho, Chiba, Chiba  
263-8522, Japan (E-mail: masakiyo@ph.chiba-u.ac.jp).  
Tel: 81-43-290-2921, Fax: 81-43-290-2921)

FEATURES  
Location/Qualifiers

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 1 (bases 1 to 1717)  
 Potter, P.M., Pawlik, C.A., Morton, C.J., Naeve, C.W. and Danks, M.K.  
 Isolation and partial characterization of a cDNA encoding a rabbit  
 liver carboxylesterase that activates the prodrug irinotecan  
 (CPT-11)  
 Cancer Res. 58 (12), 2646-2651 (1998)  
 JOURNAL  
 MEDLINE 98297515  
 PUBMED 9635592  
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 POTTER, P.M.  
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 Research Hospital, 332 North Lauderdale, Memphis, TN 38105, USA  
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 1 (bases 1 to 1975)  
 Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,K., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scherz,T.E., Brownstein,M.J., Usdin,T.B., Teshiyuki,S., Carninci,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Young,A.C., Shewchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalls,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
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 REFERENCE  
 2 (bases 1 to 1975)  
 Strausberg,R.  
 Direct Submission  
 Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>

## COMMENT

Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: DCTD/DTIP/Gazdar  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
 DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>  
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 Qy 969 CCCACTGGCTGGATGAAACCAACAGACACAGATCTCTGGTAAACTGCTGAGGGCAC 1028  
 Db 868 CTATCACTGTGGTGGTGAACCAACCAACCACTCTGCTGATGGTTCACTGCTCGGACAG 927  
 Qy 1029 TATCAGGACCAAGTGTGCTGTGTCACCAAGATGAGATTCTCCAACTGAACTTCC 1088  
 Db 928 AGACGAAGAGGAGCTCTTGGAGACGACATTTGAATGAATTTCTATCTTGGACTTAC 987  
 Qy 1089 AGAGAGACCCGGAAGAGATTTCTGGTCCATGAGCCCTGTGGTGGATGGTGGTATCC 1148  
 Db 988 AGGAGACCCCGAGAGAGATCAACCCCTTCTGGGCACTGTGATTGATGGGATGCTGCTGC 1047  
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 Db 1108 GAATTAACAAGCAGGAGTTTGGCTGGTTGATTCCAATGTTGATGAGCTATCCACTCTCG 1167  
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 Qy 1806 TCAGTCTCT 1814  
 Db 1702 CCAACCTCT 1710

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 Job time : 7763.27 secs



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OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 09:13:52 ; Search time 780.458 Seconds  
(without alignments)  
10793.891 Million cell updates/sec

Title: US-10-001-227-1  
Perfect score: 1983  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 337363 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: Geneseqn1980s:\*  
2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002s:\*  
7: Geneseqn2003as:\*  
8: Geneseqn2003bs:\*  
9: Geneseqn2003cs:\*  
10: Geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1983	100.0	1983	6	ABN84189 Human car
2	1928.6	97.3	2081	6	AAD33489 Human dru
3	1271.8	64.1	1532	5	AAS74822 DNA encod
4	1013	51.1	2456	2	AZ34105 Human PRO
5	1013	51.1	2456	3	AAC78509 Human PRO
6	1013	51.1	2456	4	AAS45953 Human DNA
7	1013	51.1	2456	7	ABX78556 Human PRO
8	1013	51.1	2456	7	ACA75528 Novel hum
9	1013	51.1	2456	7	ACA71008 Human sec
10	1013	51.1	2456	7	ACC87536 Human sec
11	1013	51.1	2456	7	ACC86922 Human sec
12	1013	51.1	2456	7	ACD04095 Human sec
13	1013	51.1	2456	7	ACA69426 CDNA enco
14	1013	51.1	2456	7	ACA90271 Novel hum
15	1013	51.1	2456	7	ACC89378 Human sec
16	1013	51.1	2456	7	ACA98169 Novel hum
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18	1013	51.1	2456	7	ACD15204 Human sec
19	1013	51.1	2456	7	ACD08791 Human sec
20	1013	51.1	2456	7	ACC96711 Human sec
21	1013	51.1	2456	7	ACF15432 Human sec
22	1013	51.1	2456	7	ACD42638 Novel hum
23	1013	51.1	2456	7	ACA72799 Human PRO

24	1013	51.1	2456	7	ACD02971	Novel hum
25	1013	51.1	2456	7	ACD01786	Novel hum
26	1013	51.1	2456	7	ACA91978	Novel hum
27	1013	51.1	2456	7	ACA63673	Novel hum
28	1013	51.1	2456	7	ACA89403	CDNA enco
29	1013	51.1	2456	7	ACA73413	Human sec
30	1013	51.1	2456	7	ACA05728	Human sec
31	1013	51.1	2456	7	ACA65562	CDNA enco
32	1013	51.1	2456	7	ACF20137	Human sec
33	1013	51.1	2456	7	ACF19523	Human sec
34	1013	51.1	2456	7	ACD21811	Human sec
35	1013	51.1	2456	7	ACF12976	Human sec
36	1013	51.1	2456	7	ACD25079	Human sec
37	1013	51.1	2456	7	ACF00128	Human sec
38	1013	51.1	2456	7	ACA72185	Novel hum
39	1013	51.1	2456	7	ACD04709	Novel hum
40	1013	51.1	2456	7	ACD18170	Human sec
41	1013	51.1	2456	7	ACD08177	Human sec
42	1013	51.1	2456	7	ACA88611	Novel hum
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44	1013	51.1	2456	7	ACD12275	Novel hum
45	1013	51.1	2456	7	ACC74190	Human sec

## ALIGNMENTS

## RESULT 1

ID ABN84189 standard; CDNA; 1983 BP.  
AC ABN84189;  
DT 23-SEP-2002 (first entry)  
DE Human carboxylesterase-2 cDNA.  
KW Carboxylesterase-2; COE-2; human; antiinflammatory; virucide; antiulcer;  
KW antiasthmatic; antirheumatic; antiarthritic; dermatological;  
KW antipsoriatic; analgesic; antitumour; cytostatic; enzyme; gene therapy;  
KW gene; ss.  
XX Homo sapiens.  
CS Homo sapiens.  
FH Key  
FT CDS  
FT Location/Qualifiers  
FT 98..1852  
FT /tag= a  
FT /product= "Carboxylesterase-2"  
FT /note= "the CDS is also specifically claimed in Claim 1"

XX WO200244357-A2.

XX 06-JUN-2002.

XX 30-NOV-2001; 2001WO-US045356.

XX 30-NOV-2000; 2000US-0250929P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Kapeller-Libermann R, Silos-Santiago I;

XX WPI; 2002-537452/57.

XX P-PSDB; ABS79484.

XX Novel isolated human carboxylesterase-2 family member polypeptide, 18903,  
XX useful for treating inflammatory disorders, pain disorders, tumor and  
XX cancer.

XX Claim 1; Page 119-122; 129pp; English.

XX The present sequence, the coding region of which is also claimed, is that  
XX of human cDNA clone Fbhi8903, which encodes carboxylesterase-2 (COE-2,

CC see ABB79484), a novel carboxylesterase family member. COB-2 participates  
 CC in the metabolism of various lipid and fatty acid compounds which are  
 CC involved in pain and/or inflammation signalling. It is highly expressed  
 CC in tissues which contain afferent neurons, particularly brain and spinal  
 CC cord tissue. The invention provides COB-2 nucleic acid molecules,  
 CC antisense nucleic acid molecules, recombinant expression vectors, host  
 CC cells, transgenic animals, isolated COB-2 proteins, fusion proteins,  
 CC antigenic peptides and anti-COB-2 antibodies. COB-2 nucleic acids are  
 CC used in claimed methods of identifying subjects having, or at risk of  
 CC developing, an inflammatory or pain disorder. Compounds capable of  
 CC treating an inflammatory or pain disorder can be identified from their  
 CC ability to modulate COB-2 nucleic acid expression or COB-2 polypeptide  
 CC activity. Modulator compounds are used in a claimed method of treating an  
 CC inflammatory or pain disorder. Carboxylesterase-associated pain disorders  
 CC include hyperalgesia, pain associated with musculoskeletal disorders and  
 CC pain associated with surgery, rheumatoid arthritis, viral infection,  
 CC allergic reaction, asthma, pancreatitis, somatoform disorders,  
 CC fibromyalgia syndrome, etc. Carboxylesterase-associated inflammatory  
 CC disorders include viral infection, ulcerative colitis, Crohn's disease,  
 CC asthma, rheumatoid arthritis, scleroderma, psoriasis, inflammatory bowel  
 CC disorder, peritonitis, chronic obstructive pulmonary disease, lung  
 CC inflammation, asthma, appendicitis, septic shock, nephritis, amyloidosis,  
 CC chronic bronchitis, sarcoidosis, scleroderma, lupus, polymyositis,  
 CC Reiter's syndrome, psoriasis, pelvic inflammatory disease, inflammatory  
 CC breast disease, orbital inflammatory disease. Other carboxylesterase-  
 CC associated disorders include tumours, cancer, aberrant blood pressure,  
 CC aberrant blood clotting, misregulation of various reproductive functions  
 CC e.g. induction of labour, and misregulation of the sleep/wake cycle. COB-  
 CC 2 nucleic acids and polypeptides are also useful in screening assays,  
 CC detection assays (e.g., chromosomal mapping, tissue typing, forensic  
 CC biology) and predictive medicine (e.g., diagnostic assays, prognostic  
 CC assays, monitoring clinical trials and pharmacogenomics)

XX Sequence 1983 BP; 460 A; 553 C; 561 G; 409 T; 0 U; 0 Other;

Query Match  
 Best Local Similarity 100.0%; Score 1983; DB 6; Length 1983;  
 Matches 1983; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCTTTAGCCAAATTCGGCCGAGGCTCCCGCCCAAGTACTTGTGGCAGGATTAAGAGCA 60  
 Db 1 CCTTTAGCCAAATTCGGCCGAGGCTCCCGCCCAAGTACTTGTGGCAGGATTAAGAGCA 60

Qy 61 GATAAAGTGTGCTACACACTGTAGACAGGCTACCATGCCATCCACAGTGTGGCATC 120  
 Db 61 GATAAAGTGTGCTACACACTGTAGACAGGCTACCATGCCATCCACAGTGTGGCATC 120

Qy 121 CACAGTGTGCCATFACCTCTGCTGCCACAGCAGGAGTGGTGGAGCATGAGTGGATTCT 180  
 Db 121 CACAGTGTGCCATFACCTCTGCTGCCACAGCAGGAGTGGTGGAGCATGAGTGGATTCT 180

Qy 181 GTGCTGAGCTCACCTCTGCTGTATGGCGCAGAGGCTTGGTGGCTTGACACCA 240  
 Db 181 GTGCTGAGCTCACCTCTGCTGTATGGCGCAGAGGCTTGGTGGCTTGACACCA 240

Qy 241 GAGCCCTCAAGTGTGTACCAAAATATGGAACCTTGCAAGGAAAACAGATGATGTGGGAA 300  
 Db 241 GAGCCCTCAAGTGTGTACCAAAATATGGAACCTTGCAAGGAAAACAGATGATGTGGGAA 300

Qy 301 GACACCATCGAAGTCTTTTAGAGTCCCTTCTCCAGACCTCTCTAGGATCTCTAG 360  
 Db 301 GACACCATCGAAGTCTTTTAGAGTCCCTTCTCCAGACCTCTCTAGGATCTCTAG 360

Qy 361 GTTTGACCTCCAGAACCCCGGAGGCTTGGAAAGGAATCAGAGATGCTACCACTACCC 420  
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Qy 421 GCCTGGTGTGCTCAGAGAGTCTGGGCGCAGCTGGGCTCGATGTAGTCAGCAGCGGGA 480  
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Qy 481 ACGGTACAAAGTGGTGGCTTACGAGGAGTCTGTGTACTGAAAGTGTACGCGCGGC 540  
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 541 GCGCGCGCGGGGATCCCAAGCTGCCAGTGTGGTCTGGTTCGGGAGCGGCTTCAT 600  
 541 GCGCGCGCGGGGATCCCAAGCTGCCAGTGTGGTCTGGTTCGGGAGCGGCTTCAT 600  
 601 CGTGGCGCTCTCTTCTCGTACGAGGCTCTGACTTGGCCCGCGCGAGAAAGTGTGCT 660  
 601 CGTGGCGCTCTCTTCTCGTACGAGGCTCTGACTTGGCCCGCGCGAGAAAGTGTGCT 660  
 661 GGTGTCTGACGACACAGGCTCGGCATCTTGGCTTCTGAGCAGCGACGACAGCAGCAGC 720  
 661 GGTGTCTGACGACACAGGCTCGGCATCTTGGCTTCTGAGCAGCGACGACAGCAGCAGC 720  
 721 GCGCGGGAACCTGGGCGGCTGTGACACAGATGGCGGCTCTGCGTGGGTGAGGAGAACAT 780  
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 781 GCGAGCTTGGGGGAGACCCAGAAATGTGACCTTGGCCAGTCSGGGGGCGCAT 840  
 781 GCGAGCTTGGGGGAGACCCAGAAATGTGACCTTGGCCAGTCSGGGGGCGCAT 840  
 841 GAGCATCTCAGACTGATGTGATGTCAACCCCTAGCCTCGGCTCTCTTCCATCGGGCCATTTC 900  
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QY 258 CCAATATGGAACCTGCAAGGAAACAGATGATGTGGGGAAGACACCCATCCAAAGTCT 317  
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QY 318 TTTTGGAGTCCCTTCTCCAGACCTCTCTAGGTATCCTCAGGTTTGCACCTCCAGAAC 377  
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QY 498 GCTTCAGCGAGGACTGTCTGTACTGAACTGTACGCGCGCGCGCGCGCGCGCGGATC 557  
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Db 1347 AGGAGCAGGTACCACTTGTGGTGGAGGATACCTGGCAATGTCAATGAGCATGACTGGA 1406  
QY 1398 AGATGCTACGAAACCGTATGATGACATAGTTCAGATGACCACTTTCGTGTATGCCACAC 1457  
Db 1407 AGATGCTACGAAACCGTATGATGACATAGTTCAGATGACCACTTTCGTGTATGCCACAC 1466  
QY 1458 TGCAGACTGCTACTACACCGAGATGCCGGCTCCTCTGTCTACCTGTATGAATTTGAGC 1517  
Db 1467 TGCAGACTGCTACTACACCGAGATGCCGGCTCCTCTGTCTACCTGTATGAATTTGAGC 1526  
QY 1518 ACCACGCTCGTGGAAATAATCGTCAAAACCCCGCACTGATGGGGCAGACCATGGGGATGAGA 1577  
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Db 1887 AGAGGGTGTTCGCCCAACCATCCAGGCCCTGGGGAGACTAGCCATGACATACCTGGGA 1946  
QY 1938 CAAGAGTTCTACCCA 1952  
Db 1947 CAAGAGTTCTACCCA 1961  
RESULT 3  
AAS74822  
ID AAS74822 standard; cDNA; 1532 BP.  
XX AAS74822;  
AC AAS74822;  
XX XX  
DT 13-FEB-2002 (first entry)  
XX  
DE DNA encoding novel human diagnostic protein #10626.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX WO200175067-A2.  
PN  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00549167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI; 2001-639362/73.

DR P-PSDB; ABG10635.  
XX New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX Claim 1; SEQ ID NO 10626; 103pp; English.  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 1532 BP; 348 A; 423 C; 441 G; 320 T; 0 U; 0 Other;  
Query Match 64.1%; Score 1271.8; DB 5; Length 1532;  
Best Local Similarity 93.5%; Pred. No. 0;  
Matches 1415; Conservative 0; Mismatches 12; Indels 86; Gaps 5;  
426 GGTGCTGCGAGGATCTCGGGGCGAGTGGCTCGATGACGTACGACGCGGGAACGGT 485  
20 GGTGCTGCGATGATCTCGGGGCGAGTGGCTCGATGACGTACGACGCGGGAACGGT 79  
486 ACAAGTGGCGCGCTTCAGCGAGGAGTCTGCTGACCTGACGAGCGTACGCGCGCGCGCG 545  
80 ACAAGTGGCTGCGCTTCAGCGAGGAGTCTGCTGACCTGACGAGCGTACGCGCGCGCGCG 139  
546 CGCCCGGGGATCCCCAGCTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 605  
140 CGCCCGGGGATCCCCAGCTCCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 199  
606 CGCGTGTCTTCTGTACAGGGCTCTGACTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 565  
200 CGCGTGTCTTCTGTACAGGGCTCTGACTTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 259  
666 TTCTGACGACAGGCTCGGCATCTTCGGCTTCTGAGCAGCGACGACGACGACGACGACGACG 725  
260 TTCTGACGACAGGCTCGGCATCTTCAGCTTCTGAGCAGCGAGCAGCAGCAGCAGCAGCAG 319  
726 GGAATCTGGGGTCTGCGACAGAT--GGCGGCTCTGCGCTGCGGTGCGAGAGAACATCGCA 784  
320 GGAATCTGGGGTCTGCGACAGATGCGCGGCTCTGCGCTGCGGTGCGAGAGAACATCGCA 379  
785 GCC--TTCCGGGGAGACCCAGG--AAATGTGACCTGTTGGCGCAGTGGCGGGGGCGCATG 841  
380 GCCTTTCGGGGAGACCCAGGGAATTTGACCTGTTGGCGCAGTGGCGGGGGCGCATG 439  
842 AGCATCTCAGAGCTGATGATGTCAACCCCTAGCTCGGGTCTCTTCCATCGGGCCATTCC 901  
440 AGCATCTCAGAGCTGATGATGTCAACCCCTAGCTCGGGTCTCTTCCATCGGGCCATTCC 499  
902 CAGAGTGGCACCCTGTTTACAGCTTTTACAGCTTTTACAGCTTTTACAGCTTTTACAGCTTT 961  
500 CAGAGTGGCACCCTGTTTACAGCTTTTACAGCTTTTACAGCTTTTACAGCTTTTACAGCTTT 559

RESULT 4  
AAZ34105  
ID AAZ34105 standard; cDNA; 2456 BP.  
XX

QY 962 AAGTTGGCCACCTGGCTGGATGCAACCAACAGCAGACAGATCCTGTTAACTGCTG 1021  
DB 560 AAGTTGGCCACCTGGCTGGATGCAACCAACAGCAGACAGATCCTGTTAACTGCTG 619  
QY 1022 AGGGCAC--TATCAGGGACCAAGGTGATGCGTGTGTCCAAACAGATGAGATCTCTCCAACT 1080  
DB 620 AGGGCACTTATCAGGGACCAAGGTGATGCGTGTGTCCAAACAGATGAGATCTCTCCAACT 679  
QY 1081 GAATTCACAGAGACCCGGAAGAGATTATCTGTCATGAGCCCTGTGTTGGATGGTGT 1140  
DB 680 GAATTCACAGAGACCCGGAAGAGATTATCTGTCATGAGCCCTGTGTTGGATGGTGT 739  
QY 1141 GGTGATCCAGATGACCCCTTTGGTGTCTCTGACCCAGGGGAAGGTTTTCATCTGTGCCCTA 1200  
DB 740 GGTGATCCAGATGACCCCTTTGGTGTCTCTGACCCAGGGGAAGGTTTTCATCTGTGCCCTA 799  
QY 1201 CTTCTAGGTGTCAACAACTGGAAATTCATTTGCTCTTTCCTTATATATGAAGTTCC 1260  
DB 800 CTTCTAGGTGTCAACAACTGGAAATTCATTTGCTCTTTCCTTATATATGAAGTTCC 859  
QY 1261 GCTAAACCGGAGCGGATGAGAAAGGAACCATCACTAAGATGCTCTGGAGTACCCGAC 1320  
DB 860 GCTAAACCGGAGCGGATGAGAAAGGAACCATCACTAAGATGCTCTGGAGTACCCGAC 919  
QY 1321 CTTGTT-----GAATATCAACCAAGCAGCAGGTACCACTGTTGGGCGCCACC 1326  
DB 920 CTTGTTGGGCGCCCTGAGCATGGATCCCAAGTCACTGTTGGGCGCCACC 979  
QY 1327 -----GAATATCAACCAAGCAGCAGGTACCACTGTTGGGCGCCACC 1359  
DB 980 TCTGCCCAGCTGGCACCAGGCTCAGATATCACCAGGAGCAGGTACCACTGTTGGT 1039  
QY 1360 GGAGGAGTACCTGGACAAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTATGAT 1419  
DB 1040 GGAGGAGTACCTGGACAAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTATGAT 1099  
QY 1420 GGAATAGTTCAAGATGSCACTTTCTGTATGCCACACTGCAGACTGCTCACTACCCG 1479  
DB 1100 GGAATAGTTCAAGATGSCACTTTCTGTATGCCACACTGCAGACTGCTCACTACCCG 1159  
QY 1480 AGATCCCGGCTCCCTGTCTACCTGTATGAATTTGAGCACCACCGCTCGTGAATAATCGT 1539  
DB 1160 AGATCCCGGCTCCCTGTCTACCTGTATGAATTTGAGCACCACCGCTCGTGAATAATCGT 1219  
QY 1540 CAAACCCGCACTGATGGGGCAGACCATGCGGATGAGATGATCTCTTTGGGGGCCC 1599  
DB 1220 CAAACCCGCACTGATGGGGCAGACCATGCGGATGAGATGATCTCTTTGGGGGCCC 1279  
QY 1600 CTTGCCACAGGCTTTCCATGGGTAGGAGAAGGCACTTAGCCTCCAGATGATGAATA 1659  
DB 1280 CTTGCCACAGGCTTTCCATGGGTAGGAGAAGGCACTTAGCCTCCAGATGATGAATA 1339  
QY 1660 CTGGGCCAACTTTGCCCGCACAGGAACCCCAATGATGGGAATCTGCCCTGCTGCCACG 1719  
DB 1340 CTGGGCCAACTTTGCCCGCACAGGAACCCCAATGATGGGAATCTGCCCTGCTGCCACG 1399  
QY 1720 CTACAAAGAGATGAAAAGTACCTGCGTGGATTTTACCAAGAGTGGGCATGAAGCT 1779  
DB 1400 CTACAAAGAGATGAAAAGTACCTGCGAGTGGATTTTACCAAGAGTGGGCATGAAGCT 1459  
QY 1780 CAAAGAGAGAGAGATGGCTTTTGGATGAGTCTGTACAGTCTCAAAAGACCTGAGAAGCA 1839  
DB 1460 CAAAGAGAGAGAGATGGCTTTTGGATGAGTCTGTACAGTCTCAAAAGACCTGAGAAGCA 1519  
QY 1840 GAGGCAATCTTAA 1852  
DB 1520 GAGGCAATCTTAA 1532

AC AA234105;  
 XX 07-DEC-1999 (first entry)  
 XX Human PRO873 nucleotide sequence.  
 DE Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
 KW secreted protein; transmembrane protein; ss.  
 XX Homo sapiens.  
 OS WO9946281-A2.  
 FN 16-SEP-1999.  
 XX 08-MAR-1999; 99WO-US005028.  
 XX 10-MAR-1998; 98US-0077450P.  
 PR 11-MAR-1998; 98US-0077632P.  
 PR 11-MAR-1998; 98US-0077641P.  
 PR 11-MAR-1998; 98US-0077649P.  
 PR 12-MAR-1998; 98US-0077791P.  
 PR 13-MAR-1998; 98US-0078004P.  
 PR 17-MAR-1998; 98US-00040220.  
 PR 20-MAR-1998; 98US-0078886P.  
 PR 20-MAR-1998; 98US-0078910P.  
 PR 20-MAR-1998; 98US-0078936P.  
 PR 20-MAR-1998; 98US-0078939P.  
 PR 25-MAR-1998; 98US-0079294P.  
 PR 26-MAR-1998; 98US-0079656P.  
 PR 27-MAR-1998; 98US-0079663P.  
 PR 27-MAR-1998; 98US-0079664P.  
 PR 27-MAR-1998; 98US-0079689P.  
 PR 27-MAR-1998; 98US-0079728P.  
 PR 27-MAR-1998; 98US-0079786P.  
 PR 30-MAR-1998; 98US-0079920P.  
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 PR 01-APR-1998; 98US-0080327P.  
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 PR 15-APR-1998; 98US-0081955P.  
 PR 21-APR-1998; 98US-0082568P.  
 PR 21-APR-1998; 98US-0082569P.  
 PR 22-APR-1998; 98US-0082700P.  
 PR 22-APR-1998; 98US-0082704P.  
 PR 23-APR-1998; 98US-0082804P.  
 PR 23-APR-1998; 98US-0082767P.  
 PR 23-APR-1998; 98US-0082796P.  
 PR 27-APR-1998; 98US-0083336P.  
 PR 28-APR-1998; 98US-0083322P.  
 PR 29-APR-1998; 98US-0083392P.  
 PR 29-APR-1998; 98US-0083495P.  
 PR 29-APR-1998; 98US-0083496P.  
 PR 29-APR-1998; 98US-0083499P.  
 PR 29-APR-1998; 98US-0083500P.  
 PR 29-APR-1998; 98US-0083545P.  
 PR 29-APR-1998; 98US-0083554P.  
 PR 29-APR-1998; 98US-0083558P.

PR 29-APR-1998; 98US-0083559P.  
 PR 30-APR-1998; 98US-0083742P.  
 PR 05-MAY-1998; 98US-0084366P.  
 PR 06-MAY-1998; 98US-0084414P.  
 PR 06-MAY-1998; 98US-0084441P.  
 PR 07-MAY-1998; 98US-0084598P.  
 PR 07-MAY-1998; 98US-0084600P.  
 PR 07-MAY-1998; 98US-0084627P.  
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 PR 15-MAY-1998; 98US-0085573P.  
 PR 15-MAY-1998; 98US-0085579P.  
 PR 15-MAY-1998; 98US-0085580P.  
 PR 15-MAY-1998; 98US-0085582P.  
 PR 15-MAY-1998; 98US-0085689P.  
 PR 15-MAY-1998; 98US-0085697P.  
 PR 15-MAY-1998; 98US-0085700P.  
 PR 15-MAY-1998; 98US-0085704P.  
 PR 18-MAY-1998; 98US-0086023P.  
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 PR 22-MAY-1998; 98US-0086414P.  
 PR 22-MAY-1998; 98US-0086430P.  
 PR 22-MAY-1998; 98US-0086486P.  
 PR 28-MAY-1998; 98US-0087038P.  
 PR 28-MAY-1998; 98US-0087106P.  
 PR 28-MAY-1998; 98US-0087208P.  
 PR 30-JUL-1998; 98US-0094651P.  
 PR 11-SEP-1998; 98US-0100038P.  
 XX (GETH ) GENENTECH INC.  
 XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
 PI WPI; 1999-551358/46.  
 XX P-FSDB; AA41723.  
 DR New secreted and transmembrane polypeptides and their polynucleotides,  
 DR useful for treating blood coagulation disorders, cancers and cellular  
 DR adhesion disorders.  
 PS Claim 2; Fig 90; 530pp; English.  
 XX The present invention describes secreted and transmembrane polypeptides  
 CC and their polynucleotides. The nucleotide sequences are useful as sources  
 CC of probes, primers, for chromosome mapping, and for generation of  
 CC antisense sequences. They can also be used to create transgenic animals.  
 CC The proteins can be used to treat a variety of diseases and disorders,  
 CC depending on their function. Diseases that may be treated include blood  
 CC coagulation disorders, cancers and cellular adhesion disorders. They may  
 CC also be used to raise antibodies. AA233891 to AA234338, and AA41685 to  
 CC AA41774 represent polynucleotide and polypeptide sequence given in the  
 CC exemplification of the present invention  
 XX Sequence 2455 BP; 528 A; 719 C; 666 G; 543 T; 0 U; 0 Other;  
 SQ  
 Query March 51.1%; Score 1013; DB 2; Length 2456;  
 Best Local Similarity 78.2%; Pred. No. 6.6e-254;  
 Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;  
 QY 224 GGTGCTTGACACCAAGAGGCTCAAGTGGTCCACCAATATGGAACCTTCGAAGGAAA 283  
 Dd 388 GGTGCTTGACACCAAGAGGCTCAAGTGGTCCACCAATATGGAACCTTCGAAGGAAA 447  
 QY 284 CAGATGATGTGGGGAAGACACCATCAAGTCTTTTAGGAGTCCCTTCTCAGACCT 343  
 Dd 448 CAGATGATGTGGGGAAGACACCATCAAGTCTTTTAGGAGTCCCTTCTCAGACCT 507  
 QY 344 CCTCTAGGTATCCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGA 403



508	Db	 CCTCTAGGTTATCCTCAGGTTTGACACTCCAGAACCCCGGAGCCCTGGAAAGAAATCAGA	567
404	QY	 GATGCTACCACTTACC CGGCTG	425
568	Db	 GATGCTACCACTTACC CGGCTGGATGGAGTCTCGCTCTGTGCGCAGGCTGGAGTCAGATG	627
426	QY	----- -----	425
628	Db	 GCAGATCTCGGCTCACTGCAACCTCGGCTCCGGGTTCAACGAGTCTCTCTGCTCTCAG	687
426	QY	----- -----GGTGCCTGCAGAGTCTCTGGGGCCAGCTGGCCCTCGATG	463
688	Db	 CCTCTAGTGTCTGGGGCTTACAGGTGCCTGCAGAGTCTCTGGGGCCAGCTGGCCCTCGATG	747
464	QY	 TAGCTCAGCACGCGGAAACGTTAAAGTGGCTCGCTTTCAGCGAGGACTGTCTGTACCTG	523
748	Db	 TACGT CAGCACGCGGAAACGTTAAAGTGGCTCGCTTTCAGCGAGGACTGTCTGTACCTG	807
524	QY	 AAGCTGTACGCGCGCGCGCGCGCGCGCGGGATCCCGAGCTGCCAGTGATGTCCTGGTTC	593
808	Db	 AAGCTGTACGCGCGCGCGCGCGCGCGGGATCCCGAGCTGCCAGTGATGTCCTGGTTC	867
584	QY	 CCGGGAGGGCCCTTCATCTCGTGGCGGTGCTTCTTCGTACGAGGCTCTGACTTGGCGCGC	643
868	Db	 CCGGGAGGGCCCTTCATCTCGTGGCGGTGCTTCTTCGTACGAGGCTCTGACTTGGCGCGC	927
644	QY	 CGCGAGAAAGTGCTGTGTGTTTCTGCAGCA CAGGCTCGGCACTCTTGGGCTTCTCTGAGC	703
928	Db	 CGCGAGAAAGTGCTGTGTGTTTCTGCAGCA CAGGCTCGGCACTCTTGGGCTTCTCTGAGC	987
704	QY	 ACGGACGACAGCCAGCGCGCGGAACTGGGGCTGCTGGACCAGATGGCGGCTCTGCGC	763
988	Db	 ACGGACGACAGCCAGCGCGCGGAACTGGGGCTGCTGGACCAGATGGCGGCTCTGCGC	1047
764	QY	 TGGGT CAGAGAAATTCGACGCTTGGGGGAGACCCAGGAAATGTGACCCCTGTTGCGC	823
1048	Db	 TGGGT CAGAGAAATTCGACGCTTGGGGGAGACCCAGGAAATGTGACCCCTGTTGCGC	1107
824	QY	 CAGTCGGCGGGGCCATGACATCTCAGGACTGATGTGCACCCCTAGGCTCGGGTCTC	883
1108	Db	 CAGTCGGCGGGGCCATGACATCTCAGGACTGATGTGCACCCCTAGGCTCGGGTCTC	1167
884	QY	 TTCACATCGGGCCATTTCCAGAGTGGCACCGCGTTATTCAGACTTTTTCATCACTAGTAAC	943
1168	Db	 TTCACATCGGGCCATTTCCAGAGTGGCACCGCGTTATTCAGACTTTTTCATCACTAGTAAC	1227
944	QY	 CCACTGAAAGTGCGCAAGAAAGTTGCCACTCTGGCTGGATGCAACCAACAGCACACAG	1003
1228	Db	 CCACTGAAAGTGCGCAAGAAAGTTGCCACTCTGGCTGGATGCAACCAACAGCACACAG	1287
1004	QY	 ATCCTGTAACTGCCTGAGGGCACTATCAGGAGCAAGAGTGTGCTGTGCCAACAG	1063
1288	Db	 ATCCTGTAACTGCCTGAGGGCACTATCAGGAGCAAGAGTGTGCTGTGCCAACAG	1347
1064	QY	 ATGAGATTCCTCCAACCTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGC	1123
1348	Db	 ATGAGATTCCTCCAACCTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGC	1407
1124	QY	 CCTGTGTGTGATGGTGTGGTGATCCACAGATGACCCCTTGGTGTCTCTGACCCAGGGGAG	1183
1408	Db	 CCTGTGTGTGATGGTGTGGTGATCCACAGATGACCCCTTGGTGTCTCTGACCCAGGGGAG	1467
1184	QY	 GTTTTCATCTGTGCCCTACCTTCTAGGTGTCAACAAACCTGGAATTCATTTGGCTCTTGCCT	1243
1468	Db	 GTTTTCATCTGTGCCCTACCTTCTAGGTGTCAACAAACCTGGAATTCATTTGGCTCTTGCCT	1527
1244	QY	 TATATCATGAGTTCCCGCTTAACCCGCGAGGCGATGAGAAAGGAACCATCACTAAGATG	1303
1528	Db	 TAT	1530
1304	QY	 CTCTGGAGTACCCGACCCCTGTTGAAATATCACCAAGGAGCAGGTACCACTTGTGGTGAG	1363

Db	1531	-----AATATCACCAGGAGCAGGTACCACTTTGTGGTGAG	1566
Qy	1364	GAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAACCCTATGATGGAC	1423
Db	1567	GAGTACCTGGACAATGTCAATGAGCATGACTGGAAGATGCTACGAACCCTATGATGGAC	1626
Qy	1424	ATAGTTCAGAATGCCACTTTTCGTGTATGCACACTGCAGACTGCTACTACCAACCGAGAT	1483
Db	1627	ATAGTTCAGAATGCCACTTTTCGTGTATGCACACTGCAGACTGCTACTACCAACCGA---	1683
Qy	1484	GCGGCCCTCCCTGTCTACCTGTATGAATTTGAGCACCACGCTCGTGGATAATCGTCAAA	1543
Db	1684	-----	1683
Qy	1544	CCCCGCACCTGATGGGGCAGACCATGGGGATGAGATGTACTTCCTTTTGGGGCCCCCTTC	1603
Db	1684	-----	1683
Qy	1604	GCCACAGGCCCTTCCATGGGTAGGAGAAAGGCACCTTAGCCCTCCAGATGATGAATACTGG	1663
Db	1684	-----	1683
Qy	1664	GCCAACTTTGCCCGCACAGGAAACCCCAATGATGGGAATCTGCCCTGCTGCCACCGCTAC	1723
Db	1684	-----GAAACCCCAATGATGGGAATCTGCCCTGCTGCCACCGCTAC	1724
Qy	1724	AACAAGGATGAAAAGTAGCTACCTGCAGCTGGATTTTACCACAAGATGGGCATGAAGCTCAAG	1783
Db	1725	AACAAGGATGAAAAGTAGCTACCTGCAGCTGGATTTTACCACAAGATGGGCATGAAGCTCAAG	1784
Qy	1784	GAGAAGAAGATGGCTTTTGGTAGTCTGTACCAAGTCTCAAGACCTGAGACGACGAGG	1843
Db	1785	GAGAAGAAGATGGCTTTTGGTAGTCTGTACCAAGTCTCAAGACCTGAGACGACGAGG	1844
Qy	1844	CAATTCCTAAGGGTGGCTATGCAGAAAGGAGCCAAAGAGGGGTTTGGCCCCCACCATTCCAGG	1903
Db	1845	CAATTCCTAAGGGTGGCTATGCAGAAAGGAGCCAAAGAGGGGTTTGGCCCCCACCATTCCAGG	1904
Qy	1904	CCCTGGGGAGACTAGCCATGGACATACCTCGGGGCAAGAGTTCTTACCCA	1952
Db	1905	CCCTGGGGAGACTAGCCATGGACATACCTCGGGGCAAGAGTTCTTACCCA	1953

## RESULT 5

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 ID AAC78509 standard: cDNA: 2456 BP.

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DT 08-FEB-2001 (first entry)

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Human PRO873 (INO440) nucleotide sequence SEQ ID NO:253.

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HUMAN FROM 73

XX Human: 60040000

**KW** Human; sex  
**KW** Person; sex  
**KW** Person; sex

WY  
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2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2818

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PD 14-SEP-2000.

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18-FEB-2000; 2000WO-US004341.  
PF

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Db 1684 ----- 1683  
 QY 1664 GCCAATTTCCCGCAGAGAAACCCCAATGATGGGAATCTGCCCTGTGGCCAGCTAC 1723  
 Db 1684 -----GAAACCCCAATGATGGGAATCTGCCCTGTGGCCAGCTAC 1724  
 QY 1724 AACAAAGATGAAAGTACCTGCAAGTGGATTTTACCACAAAGAGTGGGCATGAAGTCTCAAG 1783  
 Db 1725 AACAAAGATGAAAGTACCTGCAAGTGGATTTTACCACAAAGAGTGGGCATGAAGTCTCAAG 1784  
 QY 1784 GAGAAGAAGATGCTTTTGGATGATGCTGTGACAGTCTCAAGAGCTCAAGAGAGAGAGG 1843  
 Db 1785 GAGAAGAAGATGCTTTTGGATGATGCTGTGACAGTCTCAAGAGCTCAAGAGAGAGAGG 1844  
 QY 1844 CAATTTCAAGGGTGGCTATGACAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1903  
 Db 1845 CAATTTCAAGGGTGGCTATGACAGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1904  
 QY 1904 CCTGGGGAGACTAGCCATGGACATACCTGGGGACAAAGAGTTCTACCCA 1952  
 Db 1905 CCTGGGGAGACTAGCCATGGACATACCTGGGGACAAAGAGTTCTACCCA 1953

RESULT 6

AAS45953  
 ID AAS45953 standard; cDNA; 2456 BP.

XX AC AAS45953;  
 XX DT 18-DEC-2001 (first entry)  
 XX DE Human DNA encoding PRO polypeptide sequence #29.  
 XX KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss;  
 XX KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 XX KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 XX KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;  
 XX KW PCR primer.  
 XX OS Homo sapiens.  
 XX PN WO200168848-A2.  
 XX PD 20-SEP-2001.  
 XX PF 28-FEB-2001; 2001WO-US006520.

XX 01-MAR-2000; 2000WO-US0005601.  
 XX 02-MAR-2000; 2000WO-US0005841.  
 XX 03-MAR-2000; 2000US-0187202P.  
 XX 06-MAR-2000; 2000US-0186568P.  
 XX 14-MAR-2000; 2000US-0189320P.  
 XX 14-MAR-2000; 2000US-0189328P.  
 XX 15-MAR-2000; 2000WO-US006884.  
 XX 21-MAR-2000; 2000US-0190828P.  
 XX 21-MAR-2000; 2000US-0191007P.  
 XX 21-MAR-2000; 2000US-0191048P.  
 XX 21-MAR-2000; 2000US-0191314P.  
 XX 28-MAR-2000; 2000US-0192655P.  
 XX 29-MAR-2000; 2000US-0193032P.  
 XX 29-MAR-2000; 2000US-0193053P.  
 XX 30-MAR-2000; 2000WO-US0008439.  
 XX 04-APR-2000; 2000US-0194449P.  
 XX 04-APR-2000; 2000US-0194647P.  
 XX 11-APR-2000; 2000US-0195975P.  
 XX 11-APR-2000; 2000US-0196000P.  
 XX 11-APR-2000; 2000US-0196187P.  
 XX 11-APR-2000; 2000US-0196690P.  
 XX 18-APR-2000; 2000US-0198121P.  
 XX 18-APR-2000; 2000US-0198585P.  
 XX 23-APR-2000; 2000US-0199397P.

PR 25-APR-2000; 2000US-0199550P.  
 PR 25-APR-2000; 2000US-0199654P.  
 PR 03-MAY-2000; 2000US-0201516P.  
 PR 17-MAY-2000; 2000WO-US01370S.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000US-02020710.  
 PR 22-AUG-2000; 2000US-00644848.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000WO-US034956.  
 XX (GETH ) GENENTECH INC.  
 PA Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 DR WPI; 2001-602746/68.  
 DR P-PSDB; AAU29052.

XX PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumors, such as prostate and breast tumors, in mammals and to  
 PT screen for modulators of the compounds.

XX PS Claim 2; Fig 57; 774pp; English.

XX CC Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR  
 CC primers for PRO polypeptides of the invention. The sequences of the  
 CC invention can be used to detect the presence of a tumour in a mammal by  
 CC comparing the level of expression of a PRO polypeptide in a test sample  
 CC of cells from the animal and a control sample of normal cells, whereby a  
 CC higher level of expression in the test sample indicates the presence of a  
 CC tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep,  
 CC pigs, goats and rabbits but are preferably human. The polypeptides can be  
 CC used to stimulate tumour necrosis factor (TNF) alpha release from human  
 CC blood, when contacted with it. A specific polypeptide can be used to  
 CC stimulate the proliferation or differentiation of chondrocyte cells. The  
 CC PRO proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders

XX SQ Sequence 2456 BP; 528 A; 719 C; 666 G; 543 T; 0 U; 0 Other;

Query Match 51.1%; Score 1013; DB 4; Length 2456;  
 Best Local Similarity 78.2%; Pred. No. 6.6e-254;  
 Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;  
 QY 224 GGTGCTTGCACACACAGAGAGCCCTCAAGTGGTCAACCAATATGGAACCTTCAGAGAAA 283  
 Db 388 GGTGCTTGCACACACAGAGAGCCCTCAAGTGGTCAACCAATATGGAACCTTCAGAGAAA 447  
 QY 284 CAGATGATGTGGGAAGACACCCATCCAGTCTTTTAGGAGTCCCTCTTCAGACCT 343  
 Db 448 CAGATGATGTGGGAAGACACCCATCCAGTCTTTTAGGAGTCCCTCTTCAGACCT 507  
 QY 344 CCTTAGGTATCTCAGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGA 403  
 Db 508 CCTTAGGTATCTCAGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGA 567  
 QY 404 GATGCTACCACTACCCGCTG----- 425  
 Db 568 GATGCTACCACTACCCGCTGGAATGGAGTCTCCTCTGTGCCAGGCTGGAGTGCAGTG 627  
 QY 426 ----- 425  
 Db 628 GCACGATCTGGCTCACTGCAACCTCCGCGGTTCAGCGAGTCTCCTGCCTCAG 687  
 QY 426 -----GGTGCCTCAGAGAGTCTGGGGCCAGCTGGCCCTCGATG 463

Db 688 CCTCTGAGTCTCTGGGCTACAGGTGCTCTCAGAGTCTCTGGGCGCAGCTGGGCTGCTGATG 747  
Qy 464 TAGCTCAGCAGCGGGAAACGGTACAAGTGGCTCGCTTTCAGCAGAGACTGTCTGTACCTG 523  
Db 748 TAGCTCAGCAGCGGGAAACGGTACAAGTGGCTCGCTTTCAGCAGAGACTGTCTGTACCTG 807  
Qy 524 AAGCTGTACCG 583  
Db 808 AAGCTGTACCG 867  
Qy 584 CCGGAGCGCGCTTCACTGTGGCGCTGCTTCTTCTGTAGCAGGCTCTCACTTGGCGCGC 643  
Db 868 CCGGAGCGCGCTTCACTGTGGCGCTGCTTCTTCTGTAGCAGGCTCTCACTTGGCGCGC 927  
Qy 644 CGCGAGAAAGT 703  
Db 928 CGCGAGAAAGT 987  
Qy 704 ACGGACACAGCAGCAGCG 763  
Db 988 ACGGACACAGCAGCAGCG 1047  
Qy 764 TGGGTGACGAGAACTATGCGAGCGCTTTCGGGGAGACCCAGGAAATGTACCTGTTCGCGC 823  
Db 1048 TGGGTGACGAGAACTATGCGAGCGCTTTCGGGGAGACCCAGGAAATGTACCTGTTCGCGC 1107  
Qy 824 CAGTCGCGCGGGCGCATGAGCATCTCAGGACTGATGATGATGATGATGATGATGATGATGATG 883  
Db 1108 CAGTCGCGCGGGCGCATGAGCATCTCAGGACTGATGATGATGATGATGATGATGATGATGATG 1167  
Qy 884 TTCCATCGGGCCATTTCCAGAGTGGCACCGCGCTTATTCAGACTTTTCACTACTAGTAAC 943  
Db 1168 TTCCATCGGGCCATTTCCAGAGTGGCACCGCGCTTATTCAGACTTTTCACTACTAGTAAC 1227  
Qy 944 CCAGTGAAGTGGCCAGAGAGTGGCCAGCTGGCTGGATGCAACCAACAGCAGCACAG 1003  
Db 1228 CCAGTGAAGTGGCCAGAGAGTGGCCAGCTGGCTGGATGCAACCAACAGCAGCACAG 1287  
Qy 1004 ATCTGTGTAAGTGGCTGGAGGCACTATCAGGACCAAGGTGATGGTGTGTGTGTGTGTGTGTGT 1063  
Db 1288 ATCTGTGTAAGTGGCTGGAGGCACTATCAGGACCAAGGTGATGGTGTGTGTGTGTGTGTGTGT 1347  
Qy 1064 ATGAGATCTCTCAACTGAATCTTCAGAGAGACCCGAGAGATATCTGTGTGTGTGTGTGTGTGT 1123  
Db 1348 ATGAGATCTCTCAACTGAATCTTCAGAGAGACCCGAGAGATATCTGTGTGTGTGTGTGTGTGT 1407  
Qy 1124 CTTGT 1183  
Db 1408 CTTGT 1467  
Qy 1184 GTTTCATCTGTGCTTACCTTCTAGGTGTCAACACCTGGAATCAATTTGGCTCTTGGCT 1243  
Db 1468 GTTTCATCTGTGCTTACCTTCTAGGTGTCAACACCTGGAATCAATTTGGCTCTTGGCT 1527  
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XX US2003027272-A1.  
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QY	284	CAGATGCAATGGGGGAAACACCCATCCAACTCTTTTAGAGTCCCTTCTCCAGACCT	343
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QY	344	CCTCTAGTATCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGA	403
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QY	404	GATGCTACCACTACCCGCTG-----	425
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QY	426	-----	425
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QY	426	-----GGTGGCTGAGAGTCTCTGGGGCCAGCTGGGCTCGATG	463
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QY	464	TACGTACGACGCGGGAAACGTAACAAGTGGTGGCTTACGCGAGGACTGTCTGTACCTG	523
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QY	524	AACGTGTACGCGCGCGCGCGCGGCGGATCCCGAGCTGCCAGTGGTCTGGTTC	583
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QY	584	CGGAGGCGGCTTCACTGGTGGGCTGCTTCTTCGTACGAGGCTCTGACTGGCGCC	643
DB	868	CGGAGGCGGCTTCACTGGTGGGCTGCTTCTTCGTACGAGGCTCTGACTGGCGCC	927
QY	644	CGGAGGAGGTTGCTGCTGCTTCTGACGACAGGCTCCGCACTCTTCGGCTTCTGAGC	703
DB	928	CGGAGGAGGTTGCTGCTGCTTCTGACGACAGGCTCCGCACTCTTCGGCTTCTGAGC	987
QY	704	ACGAGACGACCCACGCGCGGAACTGGGGGCTGTGGACCAAGATGGCGGCTCTGCGC	763
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QY	764	TGGGTGAGGAGACATCGAGGCTTGGGGGAGACCCAGGAATGTGACCTGTTCCGC	823
DB	1048	TGGGTGAGGAGACATCGAGGCTTGGGGGAGACCCAGGAATGTGACCTGTTCCGC	1107
QY	824	CAGTCGGCGGGGCAATGAGCATCTCAGGACTGATGTACCCCTAGCCTCGGGTCTC	883
DB	1108	CAGTCGGCGGGGCAATGAGCATCTCAGGACTGATGTACCCCTAGCCTCGGGTCTC	1167
QY	884	TTCCATCGGGCCATTTCCAGAGTGGCACCGGTTATTCAGACTTTTCATCCTAGTAAC	943

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QY	944	CCACTGAAAGTGGCCAAAGAGTTGCCCACTGGTGGATGCAACCAACAGCACAG	1003
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QY	1064	ATGAGATTCCTCCAACTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGTTCCATGAGC	1123
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QY	1124	CTGTGGTGGATGGTGGTATCCAGATGACCTTTTGGTCTCTGCTGACCCAGGGAG	1183
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QY	1184	GTTTCATCTGTGCCCTACCTTCTAGGTGTCAACCACTGGAATTCATTTGGCTCTTGCT	1243
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QY	1784	GAGAGAGATGGCTTTTGGATGAGTGTGTACAGTCTCAAGACTTCAAGAGCAGAGG	1843
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XX  
DT 07-JUL-2003 (first entry)  
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KW tumour necrosis factor-alpha release; TNF-alpha release;  
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Query Match 51.1%; Score 1013; DB 7; Length 2456;
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DB 688 CCTCTGAGTGTCTGGGCTACAGGTGCTGAGGAGTCTCTGGGGCCAGTGGSCCTTCGATG 747
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DB 1531 -----AATATCAACAGGAGCAGGTACCACTTTGTGGTGGAG 1566
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QY 426 -----GGTGCTGCAGGAGTCTCGGGCCAGCTGGGCTCGATG 463
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QY	1664	GCCAACTTTGCCGCGACAGGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGTTAC	1723
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XX ACC86922;

XX AC

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DT 05-AUG-2003 (first entry)

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XX Homo sapiens.

XX US2003036159-A1.

XX 20-FEB-2003.

XX 02-JUL-2002; 2002US-00189773.

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Qy 764 TGGGTGCAGGAGAACATCGCAGCCCTCGGGGGAGACCCAGGAAATGTACACCTGTTCGGC 823
Db 1048 TGGGTGCAGGAGAACATCGCAGCCCTCGGGGGAGACCCAGGAAATGTACACCTGTTCGGC 1107

Qy 824 CAGTCGCGGGGGCCATGAGCATCTCAGGACTGATGTACCCCTAGCCTCGGTTCTC 883
Db 1108 CAGTCGCGGGGGCCATGAGCATCTCAGGACTGATGTACCCCTAGCCTCGGTTCTC 1167

Qy 884 TTCCATCGGGCCATTTCCAGAGTGGCACCGCTTATTACACTTTTTCATCACTAGTAAC 943
Db 1168 TTCCATCGGGCCATTTCCAGAGTGGCACCGCTTATTACACTTTTTCATCACTAGTAAC 1227

Qy 944 CCACCTGAAAGTGGCCAAAGGTTGCCCACTGCTGGATGCAACCAACCAAGACAG 1003
Db 1228 CCACCTGAAAGTGGCCAAAGGTTGCCCACTGCTGGATGCAACCAACCAAGACAG 1287

Qy 1004 ATCCTGTAAACTGCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTCTCAACAAG 1063
Db 1288 ATCCTGTAAACTGCTGAGGGCACTATCAGGGACCAAGGTGATGCGTGTCTCAACAAG 1347

Qy 1064 ATGAGATTCTCCAACTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGC 1123
Db 1348 ATGAGATTCTCCAACTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGC 1407

Qy 1124 CTTGTTGGTGGATGGTGGTGTATCCAGATGACCTTTGTTGCTCTACCCAGGGGAG 1183
Db 1408 CTTGTTGGTGGATGGTGGTGTATCCAGATGACCTTTGTTGCTCTACCCAGGGGAG 1467

Qy 1184 GTTTCATCTGTGCCCCCTACCTTCTAGGTGTCAACAACTGGAATTCATTTGGCTTTCGCT 1243
Db 1468 GTTTCATCTGTGCCCCCTACCTTCTAGGTGTCAACAACTGGAATTCATTTGGCTTTCGCT 1527

Qy 1244 TATATCATGAAGTTCCTCCCTAAACCGGAGGGGATGAGAAAGAAACCATCATTAGATG 1303
Db 1528 TAT----- 1530

Qy 1304 CTCTGGAGTACCCGCACTCTGTAATATCACAAGGAGCAGGTACCACTTTGTTGGTGGAG 1363
Db 1531 -----AATATCACAAGGAGCAGGTACCACTTTGTTGGTGGAG 1566

Qy 1364 GAGTACCTGGACAAATGTCAATGAGCATGACTGGAAGATGCTACGAAAACGCTATGATGAGC 1423
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Qy 1424 ATAGTTCAGAGTCCCACTTTGCTGTATGCCACACTGCAGACTGCTCACTACCCAGGAT 1483
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Qy 1604 GCCACAGGCTTTCCATGGGTAAAGGAGAGGCACTTAGCTCCAGATGATGAATACTGG 1663
Db 1684 ----- 1683

Qy 1664 GCCAACTTTGCCCGCACAGGAAACCCCAATGATGGAATCTGCCCTGTGGCCACGCTAC 1723
Db 1684 -----GAAACCCCAATGATGGAATCTGCCCTGTGGCCACGCTAC 1724

Qy 1724 AACAGGATGAAAGTACCTGAGTGGATTTTACCAAGAGTGGGATGAGTCAAGTCAAG 1783
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Db	1528	TAT-----	1530	PR	17-OCT-1997;	97US-0063486P.
Qy	1304	CTCTGGAGTACCGCACCTGTTGAATATCACCAGGAGGAGTACCACTTGTGGTGAG	1363	PR	24-OCT-1997;	97US-0063120P.
Db	1531	-----AATATCACCAGGAGGAGTACCACTTGTGGTGAG	1566	PR	28-OCT-1997;	97US-0063121P.
Qy	1364	GAGTACCTGGACAATGTCAATGAGCATGCTGGAAGATGCTACGAACCGTATGATGGAC	1423	PR	28-OCT-1997;	97US-0063540P.
Db	1567	GAGTACCTGGACAATGTCAATGAGCATGCTGGAAGATGCTACGAACCGTATGATGGAC	1626	PR	28-OCT-1997;	97US-0063544P.
Qy	1424	ATAGTTCAAGATGCCACTTGTGTATGCCACATGCTGAGACTGCTACCTACCCAGAT	1483	PR	28-OCT-1997;	97US-0063564P.
Db	1627	ATAGTTCAAGATGCCACTTGTGTATGCCACATGCTGAGACTGCTACCTACCCAGAT	1583	PR	29-OCT-1997;	97US-0063734P.
Qy	1484	GCCGCGCTCCCTGTCTACCTGTATGAATTTGAGCACCAACGCTCGTGGATAATCGTCAAA	1543	PR	31-OCT-1997;	97US-0063870P.
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Qy	1544	CCCCGCACTGATGGGCGAGACCATGGGATGAGATGACTTCTCTTTGGGGGCCCCCTTC	1603	PR	13-NOV-1997;	97US-0065311P.
Db	1684	-----	1683	PR	24-NOV-1997;	97US-0066120P.
Qy	1604	GCCACAGGCTTCCATGGTGAAGGAGAGGCACTTAGCCTCCAGATGATGAATACTGG	1663	PR	24-NOV-1997;	97US-0066466P.
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Qy	1664	GCCAACTTTGCCCGCACAGGAAACCCCAATGATGGGAATCTGCCCTGCTGCCACGCTAC	1723	PR	11-DEC-1997;	97US-0069335P.
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Db	1725	AACAGGATGAAGTACCTGCAGCTGATTTTACCAACAGAGTGGCATGAGCTCAAG	1784	PR	18-DEC-1997;	97US-0068017P.
Qy	1784	GAGAAGAGATGGCTTTTGGATGAGTCTGTACAGTCTCAAGACCTGAGAAGCAGAGG	1843	PR	10-MAR-1998;	98US-0077450P.
Db	1785	GAGAAGAGATGGCTTTTGGATGAGTCTGTACAGTCTCAAGACCTGAGAAGCAGAGG	1844	PR	11-MAR-1998;	98US-0077632P.
Qy	1844	CAATTCATAGGGTGGCTATGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1903	PR	11-MAR-1998;	98US-0077649P.
Db	1845	CAATTCATAGGGTGGCTATGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1904	PR	20-MAR-1998;	98US-0078866P.
Qy	1904	CCCTGGGAGACTAGCCATGACATACCTGGGGACAAGAGTCTTACCCA	1952	PR	27-MAR-1998;	98US-0079664P.
Db	1905	CCCTGGGAGACTAGCCATGACATACCTGGGGACAAGAGTCTTACCCA	1953	PR	31-MAR-1998;	98US-0080107P.

RESULT 13  
ACA69426  
ID ACA69426 standard; cDNA; 2456 BP.  
XX  
AC ACA69426;  
XX  
DT 27-JUN-2003 (first entry)  
XX  
DE cDNA encoding human PRO polypeptide #29.  
XX  
KW Human; PRO polypeptide; secreted and transmembrane protein; tumour;  
KW chromosome mapping; gene mapping; cytostatic; gene therapy; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN US2003032113-A1.  
XX  
PD 13-FEB-2003.  
XX  
PF 20-JUN-2002; 2002US-00176911.  
XX

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PR 10-JUN-1998; 98US-00887738P.
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PR 10-JUN-1998; 98US-0088824P.
PR 10-JUN-1998; 98US-0088825P.
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PR 25-JUN-1998; 98US-0090696P.
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PR 02-JUL-1998; 98US-0091632P.
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PR 04-AUG-1998; 98US-0095282P.
PR 10-AUG-1998; 98US-0095998P.
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PR 01-SEP-1998; 98US-0098716P.
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PR 16-SEP-1998; 98WO-US019330.
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PR 06-OCT-1998; 98US-0103258P.
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PR 07-OCT-1998; 98US-00168978.
PR 07-OCT-1998; 98US-0103395P.

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Best Local Similarity 78.2%; Pred. No. 6.6e-254;
Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;

QY 224 GGTGCTTGCACACCAGAGGCTCAAGTGTACCAATATGGAACCTCGAAGGAAA 283
DB 388 GGTGCTTGCACACCAGAGGCTCAAGTGTACCAATATGGAACCTCGAAGGAAA 447
QY 284 CAGATGCATGTGGGAAGACACCCATCCAGTCTTTTATAGGAGTCCCTTCCAGACT 343
DB 448 CAGATGCATGTGGGAAGACACCCATCCAGTCTTTTATAGGAGTCCCTTCCAGACT 507
QY 344 CCTCTAGGTATCCTCAGGTTTGACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGA 403
DB 508 CCTCTAGGTATCCTCAGGTTTGACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGA 567
QY 404 GATGCTACCACTACCCGCTG----- 425
DB 568 GATGCTACCACTACCCGCTGAGTCTGCTGTGCGCAGGCTGGAGTGCAGTG 627
QY 426 ----- 425
DB 628 GCACGATCTGGCTCACTGCAACTCCGCTCCCGGGTTCAAGCGAGTCTCCTGCTCAG 687
QY 426 -----GGTGCCTGCAGGAGTCTCGGGGCCAGCTGGCCTCGATG 463
DB 688 CCTCTAGTGTCTGGGGCTACAGGTGCTCGAGGAGTCTCGGGCCAGCTGGCCTCGATG 747
QY 464 TACGTACGACGCGGGAACGGTACAGTGGCTGGCTTACGAGGAGTCTGTACTCTG 523
DB 748 TACGTACGACGCGGGAACGGTACAGTGGCTGGCTTACGAGGAGTCTGTACTCTG 807
QY 524 AACGTGTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 583
DB 808 AACGTGTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 867
QY 584 CCGGAGGCGGCTTCACTGCTGGGCGCTGCTTCTGTTACGAGGCTCTGACTTGGCGCGCC 643

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Db 868 CCGGGAGCGCTTTCATCGTGGGCGTCTTCTTCGTACGAGGCTCTGACTTTGGCGGC 927  
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Db 928 CGCAGAAAGTGTGCTGGTGTCTCTCAGCACAGGCTCGGCATCTTCGGCTTCTTGAGC 987  
Qy 704 ACGGACACACACCGCGCGCGGAACTGGGGGCTGCTGGACAGATGGCGGCTCTGCGC 763  
Db 988 ACGGACACACCGCGCGCGGAACTGGGGGCTGCTGGACAGATGGCGGCTCTGCGC 1047  
Qy 764 TGGGTGAGAGAAATCAGACCTTCGGGGAGACCCAGGAAATGACCTTGTGCGC 823  
Db 1048 TGGGTGAGAGAAATCAGACCTTCGGGGAGACCCAGGAAATGACCTTGTGCGC 1107  
Qy 824 CAGTCGGGGGGGCGATGAGCATCTCAGGACTGATGATGTCACCCCTAGCTCGGGTCTC 883  
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Qy 884 TTCCATCGGGCCATTTCCAGAGTGGCACCGCGTTATTCAGACTTTTCATCATAGTAAC 943  
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Qy 944 CCAGTGAAGTGGCCAGAGAGTGGCCACCTGGCTGGATGCCAACACACACACACAG 1003  
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Qy 1004 ATCTGTGTAACTGCTGAGGGCACTATCAGGGACCAAGGTGATGGTGTCCAAACAG 1063  
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Db 1528 TAT----- 1530  
Qy 1304 CTCTGGAGTACCCGCACTTGTGAATATCAACAGGAGAGGTACCATTTGGTGGAG 1363  
Db 1531 -----AATATCAACAGGAGAGGTACCATTTGGTGGAG 1566  
Qy 1364 GAGTACCTGGCAATGTCAATGAGCACTGGAAGATGCTACGAACCGTATGATGGAC 1423  
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Qy 1904 CCTGGGAGAGACTAGCCATGACATACCTGGGGAACAAGAGTTCTTACCCA 1952  
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RESULT 14  
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ID ACA90271 standard; cDNA; 2456 BP.  
XX  
AC ACA90271;  
XX DT 11-AUG-2003 (first entry)  
XX  
DE Novel human secreted and transmembrane protein PR0873 cDNA.  
XX  
KW Human; gene therapy; tissue typing; tumour; chondrocyte proliferation;  
KW chondrocyte differentiation; tumour necrosis factor-alpha release; ss;  
XX affinity purification; gene.  
OS Homo sapiens.  
XX  
PN US2003036147-A1.  
XX  
PD 20-FEB-2003.  
XX  
PF 02-JUL-2002; 2002US-00187741.  
XX  
PR 18-SEP-1997; 97US-0059263P.  
PR 18-SEP-1997; 97US-0059266P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 21-OCT-1997; 97US-0063486P.  
PR 24-OCT-1997; 97US-0063120P.  
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PR 28-OCT-1997; 97US-0063540P.  
PR 28-OCT-1997; 97US-0063541P.  
PR 28-OCT-1997; 97US-0063544P.  
PR 28-OCT-1997; 97US-0063564P.  
PR 29-OCT-1997; 97US-0063734P.  
PR 31-OCT-1997; 97US-0063870P.  
PR 31-OCT-1997; 97US-0084103P.  
PR 13-NOV-1997; 97US-0085311P.  
PR 21-NOV-1997; 97US-0066120P.  
PR 24-NOV-1997; 97US-0066466P.  
PR 24-NOV-1997; 97US-0066772P.  
PR 11-DEC-1997; 97US-0069335P.  
PR 12-DEC-1997; 97US-0069425P.  
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PR 18-DEC-1997; 97US-0068017P.  
PR 10-MAR-1998; 98US-0077450P.  
PR 11-MAR-1998; 98US-0077632P.  
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PR 20-MAR-1998; 98US-0078939P.  
PR 27-MAR-1998; 98US-0079664P.  
PR 27-MAR-1998; 98US-0079786P.  
PR 31-MAR-1998; 98US-0080107P.  
PR 31-MAR-1998; 98US-0080194P.  
PR 01-APR-1998; 98US-0080327P.  
PR 01-APR-1998; 98US-0080333P.





KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
XX anthrathitic; vulnery; gene therapy; gene; ss.  
OS Homo sapiens.  
XX US2003027264-A1.  
XX 06-FEB-2003.  
XX 18-JUN-2002; 2002US-00174579.  
XX 18-SEP-1997; 97US-0059263P.  
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OM nucleic - nucleic search, using sw model

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Searched: 682709 seqs, 277475446 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	148.2	7.5	1845	1	US-07-732-962A-1
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8	148.2	7.5	2256	3	US-08-814-095-1
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## ALIGNMENTS

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; Patent No. 6107549  
; GENERAL INFORMATION:  
; APPLICANT: Feng, Paul C.C.  
; APPLICANT: Ruff, Thomas G.  
; TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via  
; TITLE OF INVENTION: Expression of Esterase Enzymes  
; FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance  
; CURRENT APPLICATION NUMBER: US/09/264,737A  
; CURRENT FILING DATE: 1999-03-09  
; EARLIER APPLICATION NUMBER: 60/077,377  
; EARLIER FILING DATE: 1998-03-10  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 1701  
; TYPE: DNA  
; ORGANISM: Rabbit  
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 ; Patent No. 6664091  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Curtis, Roy A. J.  
 ; APPLICANT: Silos-Santiago, Inmaculada  
 ; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE  
 ; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF  
 ; FILE REFERENCE: 10448-122001  
 ; CURRENT APPLICATION NUMBER: US/10/023,515  
 ; CURRENT FILING DATE: 2001-12-18  
 ; PRIOR APPLICATION NUMBER: 60/256,369  
 ; PRIOR FILING DATE: 2000-12-18  
 ; PRIOR APPLICATION NUMBER: 60/279,508  
 ; PRIOR FILING DATE: 2001-03-28  
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; Sequence 1, Application US/10023515  
; Patent No. 6664091  
; GENERAL INFORMATION:

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; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLESTERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-122001
; CURRENT APPLICATION NUMBER: US/10/023,515
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/256,369
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/279,508
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2158
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96)...(1838)
; US-10-023-515-1

Query Match      13.8%; Score 272.8; DB 4; Length 2158;
Best Local Similarity 53.0%; Pred. No. 1.1e-64;
Matches 812; Conservative 0; Mismatches 627; Indels 93; Gaps 7;

QY      305 CCCATCCCAAGTCTTTTAGGAGTCCCTTCTCCAGACCTCTCTAGGTATCTCTAGGTTT 364
Db      270 CCTGTGAAGTGTCTCTCGAGTCCCTTGTGCTGCCCTGGGATCCTCTGCGATT 329
QY      365 GCACCTCCAGAACCCCGAGCCCTGGAAGAAATCAGAGATGCTTACCACTTACCCGCT 424
Db      330 ACGAACCCGACCTGCATCGCCCTGGGATAACTTGGAGAACCCCTCTCTACCCCTAAT 389
QY      425 GAGTGGCTCAGAGTCTCTGGGGCCAGCTGGCTCGATGTCAGTCAGCACCGGGAACGG 484
Db      390 TTGTGCTCCAGAACTCAGAGTG---GCTGCTCTTAGATCAACATGCTCAAGTGGAT 446
QY      485 TACAAGTGGCTCGCTTTCAGCAGGACTGTCTGTACTCAACGCTGTACGCGCGCGCGC 544
Db      447 TACCGAATTCGGAGTGTCAAGACTGCTCTACTTGAACATCTATGGCTGCCAC 506
QY      545 GGGCCCGGGGATCCCGAGTGCAGTGCAGTGTGTTCCCGGAGGCGCTTCACTG 604
Db      507 GCGCATACAGGCTCCAAAGCTCCCGTCTTGGTGTGTTCCAGGAGGTGCTTCAAGACT 566
QY      605 GCGCTGCTTCTGTACGAGGCTCTGACTTGGCGCGCGCGGAGAAAGTGTGCTGGTG 664
Db      567 GGTACGCTCCATCTTTGATGGTCCGCCCTGGCTGCTATGAGGACGCTGCTGTG 626
QY      665 TTTCTGACACAGGCTCGCATCTTCGGCTTCTTGAGCAGGAGCAGCAGCCACCGCGCC 724
Db      627 GTCGTCCAGTACCGGCTAGGAATATTGTTTCTTCAACATGCGGATCAGCATGCTCG 686
QY      725 GGAACCTGGGGCTCTGGACCCAGATGGCGCTCTGCGTGGTGCAGGAGAACATCGCA 784
Db      687 GGAACCTGGGGCTTCAAGGACAGGTTGCTGCTGCTTGGCGAGTCCCGGAGGCTAAGT 746
QY      785 GCCTTCGGGGAGACCCAGAAATGTACCTTTCGGCCAGTCTGGCGGGGCGCCATGAGC 844
Db      747 TTTCTGGTGGGACCCAGCTCTGTGACCACTTTTGGCGAGTCCCGGAGGCTAAGT 806
QY      845 ATCTCAGGACTGATGATGTCACTTGGCTCTTCCATCGGCGGCTTCCAG 904
Db      807 GTTCTAGTCTTATCTGCTCCCATGGCCAAAGGCTTATCCCAAGACCATCATGGAG 866
QY      905 AGTGGCACCGCGTTATTTCAGACTTTTTCATCACTAGTAACTCCACTGA-----AAGTGGCC 958
Db      867 AGTGGGTGGCCATCATCTTACCTGGAGGCCCATGATTATGAGAGAGTGGACCTG 926
QY      959 AAGAAGTTGCCACCTGGCTGATGCAACCAACAGCAGCAGATCTCTGTTAACTGC 1018
Db      927 CAGGTGTTGCACATTTCTGTGTAACTTCAATGCGTCAGACTCTGAGGCCCTCTGTGAGTGC 986

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QY 896 ATTTCACAGTGG-----CACGGCTTATTCAGACTTTTTCATCTACTAGTACCCACTG 949
Db 769 GTGCTGACAGCGGTGCCCCCAATGGACCTTGGCCACGGTGGGCATGGAGAGGCCGT 828
QY 950 AAAGTGGCCAGAGGTGGCCACTGGCTGGTGGATGCAACACACACACACACAGATCTTG 1009
Db 829 CGCAGGCCACGACGCTGGCCACTTGTGGCTGTCTCCAGGCGGCACTGGTGGGAAT 888
QY 1010 GTAACCTGCTGAGGGCACTATCAGGACCAAGGTGATGCTGTGTCCAAACAGATGAGA 1069
Db 889 GACACAGCTGGTAGCTGCTTCGGACACAGCAGCGCAGGTCTCTGGTGAA----- 941
QY 1070 TTCTCCCACTGAATTCACAGAGACCCCGAAGAGATTATCTGGTCCATGAGCCCTGTG 1129
Db 942 --CCAGAAATGGACAGTGCCTCAAGAAAGCGTCTTCGGGTCTCTCGTGGCTGTG 999
QY 1130 GTGATGGTGTGGTATCCAGATGACCTTTGGTCTCTGTGACCCAGGGAAGTTTCA 1189
Db 1000 GTAGTGGAGACTTCCTCAGTGACACCCAGAGGCCCTCATCAACGGGAGACTTCCAC 1059
QY 1190 TCTGTGCCCTACCTTCTAGTGTCAACAACTGGAATTCATTTGGTCTTTCCTTATATC 1249
Db 1060 GGCCTGCAGGTGTGGTGGTGGTGAAGATGAGGCTCGTATTTCTGGTTTACGGG 1119
QY 1250 ATGAAGTTCCGGCTAAACCGCGAGCGATGAGAAAGAAACCATCATTAAGATGCTCTGG 1309
Db 1120 GCCCAGGCTTCAGCAAGACACAGCTCTCTCATCAGCCGCGCGAGTTCTTGGCCGGG 1179
QY 1310 AGTACCCGCACTCTTGAATATACCAAGAGCAGGTACCTTTGGTGGTGGAGGAGTAC 1369
Db 1180 GTGGGTGGGTTCCTCCAGTTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1239
QY 1370 CTGACCAATGTCAATGACATGACTGGAAGATGCTGGAAGATGCTGGAAGATGCTGGA 1429
Db 1240 ACAGCTGGGTGATCCCGAGGACCCGCGACGCTGAGGAGGCGCTTGGATGTGGTG 1299
QY 1430 CAAGTCCGCTTTCTGGTATGACACTGCAGACTGCTCACTACCAACCGAGATCGCGC 1489
Db 1300 GGCACCAATGTCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1359
QY 1490 CTCCTGTCTACCTGTATGAATTTGAGCAACACGCTCGTGGAAATATCGTCAAAACCCCGC 1549
Db 1360 GCCCGGTGTACGCTACGTTCTTTGAACACCGTGC---TTCCAGCTCTCTCGGCCCTG 1416
QY 1550 ACTGATGGGCGACACCATGGGATGAGATGCTACTTCTCTTTGGGGCCCTT---CGCC 1606
Db 1417 TGSATGGGGTGGCCCGCTACGATCGAGATCGAGTTCTCTTGGGATCCCGCTGGACCCC 1476
QY 1607 ACAGGCTCTTCCATGGGTAGGAGAGGCACTTAGCCTCCAGATGATGAATATCTGGGCC 1666
Db 1477 TCTGAACTACACGGCAGAGGAGAAATCTTCCGCCAGCGACTGATGCGATCTGGGCC 1536
QY 1667 AACTTTGGCCGACAGGAACCCCAATGA 1695
Db 1537 AACTTTGGCCGACAGGGGATCCCAATGA 1565
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RESULT 5
PCT-US92-06106-1
; Sequence 1, Application PC/TUS9206106
; GENERAL INFORMATION:
; APPLICANT: Fischer, Meir
; TITLE OF INVENTION: ENZYMATICALLY ACTIVE RECOMBINANT HUMAN
; TITLE OF INVENTION: ACETYLCHOLINESTERASE AND USES THEREOF
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White, Esq.
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/06106
; FILING DATE: 19920722
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 39304-B-PCT/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1845 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1842
; PCT-US92-06106-1
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Query Match 7.5%; Score 148.2; DB 5; Length 1845;
Best Local Similarity 48.3%; Pred. No. 1.3e-30;
Matches 890; Conservative 0; Mismatches 693; Indels 36; Gaps 8;

QY 305 CCCATCCAAAGTCTTTTATAGGAGTCCCTTCTCCAGACCTCTCTAGGTATCTCTAGGTTT 364
Db 175 CTTGTCTCTGCTTTCTGGCATCCCTTTGGGAGCCACCCATGGGACCCGCTGCTTT 234
QY 365 GCACCTCCAGAGCCCGGAGCCCTGGAAGAAATCAGAGATGCTACCACTTACCCTGCT 424
Db 235 CTGCCACCGGACCCCAAGAGCTTTGTCAGGGTGGTAGAGCTTAACTTCCAGAGT 294
QY 425 GGGTGCCTGCAGAGTCTCTGGGGCCAGCTGGCTCGATGTACGTGACGACCGGGAAACGG 484
Db 295 GTCTGCTACCAATATGT---GGACACCTATATACCCAGGTTTGGAGGACACCGAGATGG 351
QY 485 TACAAGTGGCTGGCTTTCAGCGAGGACTGCTGTACTCTGAACGTGTACGCGCGCGCGC 544
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QY 545 GCGCCCGGGGATCCCGAGTGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 604
Db 412 CGGCC---TACATCCCGCCACCTGCTCTCTGATCTATGGGGTGGCTTCTACAGT 468
QY 605 GCGCTGCTTCTT-----CGTACAGGGCTCTGACTTGGCCGCGCCCGGAGAGAGTGGTG 658
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QY 659 CTGGTGTCTTCTGACACAGGCTCGGCATCTTGGCTTCTTGGTACACGACGACACAGCC-- 716
Db 529 CTGGTGTCCATGAATACCGGTGGAGCTTGTGCTTCTGGCCCTGCCGGGAGCCGA 588
QY 717 -ACGCGCGGGAACTGGGGGCTGTGACACAGATGGGGCTCTGCGGTGGTGGTGGAGAG 775
Db 589 GAGGCGCGGGCAATGTGGGTCTCTGGATCAGAGGCTGGCCCTGCACTGGGTGGAGAG 648
QY 776 AACATCGAGCTTCGGGGGAGACCCAGGAAATGTGACCTGTTCCGGCCAGTTCGGCGGG 835
Db 649 AACGTGGAGCTTCGGGGGTGACCCGACATCAGTACGCTGTTTGGGGAGAGCCGCGGA 708
QY 836 GCCATGAGCATCTCAGGACTGATGATGTACCCCTAGCTCGGGTCTCTTCCATCGGCC 895
Db 709 GCGGCTCGGTGGGATGCACCTGCTGTCCCGCCGACCGCGGGGCTGTTCACAGGGCC 768
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QY 856 ATTTCCAGAGTGG-----CACCGGTGTTTACAGACTTTTCATCACTAGTAACCCACTG 949  
 Db 769 GTGCTGCAGAGCGGTGCCCCCAATGGACCTTGGGCCACGGTGGGCATGGGAGAGGCCCGT 828  
 QY 950 AAAGTGGCCAAAGAGTTGCCCACTGGCTGGATGCAACACACACACACACACAGATCCTG 1009  
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 Db 889 GACACAGAGCTGGTAGCTGCTTCCGACACAGCAGCGCAGGTCTTGGTGA----- 941  
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 Db 1000 GTAGATGAGACTTCTCAGTGACACCCAGAGCCCTCATCAACGGCGGAGACTTCCAC 1059  
 QY 1190 TCTGTCCTACCTTCTAGGTGTCAACAACTGGAATCAATTGGCTCTTGCCTTATATC 1249  
 Db 1060 GGCCTGACGTGCTGGTGTGGTGTGAAGATGAGGCTGTATTTCTGTTTACGGG 1119  
 QY 1250 ATGAAGTTCCCGCTAAACCGGACGGATGAGAAAGAAACCATCACTAAGATGCTCTGG 1309  
 Db 1120 GCGCCAGGCTTCAGCAAAAGACAGAGTCTCTCATCAGCGGCGGAGTTCTTGGCGGG 1179  
 QY 1310 AGTACCCGACCTTTCATATATCACCAGAGCAGGTACCACTTGGTGGAGGATAC 1369  
 Db 1180 GTGCGGTGCGGGTTCCTCCAGGTAAAGTGA CTTGCACCCAGAGCTGTGGTCTGCATTAC 1239  
 QY 1370 CTGGACAATGTCAATGAGCATGACTGGAAGATGTACAAACCGTATGATGACATAGTT 1429  
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 Db 1537 AACTTTGCCGACAGGAGATCCCAATGA 1565

RESULT 6

US-08-318-826A-5  
 ; Sequence 5, Application US/0831826A  
 ; Patent No. 5891725  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sored, Hermona  
 ; APPLICANT: Zakut, Haim  
 ; APPLICANT: Eckstein, Fritz  
 ; TITLE OF INVENTION: Synthetic Antisense  
 ; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Kohn & Associates  
 ; STREET: 30500 No. 5891725thwestern Hwy., Suite 410  
 ; CITY: Farmington Hills

STATE: Michigan  
 COUNTRY: US  
 ZIP: 48334  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING: IBM PC compatible  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA: US/08/318,826A  
 FILING DATE:  
 CLASSIFICATION: 514  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kohn, Kenneth I.  
 REGISTRATION NUMBER: 30,955  
 REFERENCE/DOCKET NUMBER: 2391.00001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (248) 539-5050  
 TELEFAX: (248) 539-5055  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2256 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 FEATURE:  
 OTHER INFORMATION: /note= "splice variant: Exons 1, 2,  
 OTHER INFORMATION: 3, 4 and 6"  
 US-08-318-826A-5

Query Match 7.5%; Score 148.2; DB 2; Length 2256;  
 Best Local Similarity 48.3%; Pred. No. 1.4e-30;  
 Matches 680; Conservative 0; Mismatches 693; Indels 36; Gaps 8;

QY 305 CCCATCCAAAGCTTTTAGGAGTCCCTCTTCCAGACCTCTCTAGTATCTCTCAGGTTT 364  
 Db 334 CTTGTCTCTGCTTTCTTCTGGCATCCCTTTTGGGAGCCACCCATGGGACCCCTCGCTTT 393  
 QY 365 GCACCTCCAGAACCCCGGAGCCTGGAAAGGATCAGAGATGCTACCACTACCGCCT 424  
 Db- 394 CTGCCACCGGAGCCCAAGCAGCTTGGTCAGGGTGGTAGACGCTCAACCTTCCAGAT 453  
 QY 425 GGTGCTCTGCAGGAGTCTCTGGGGCCAGCTGGCTCGATGTACGTACGACGCGGGAACGG 484  
 Db 454 GTCTGTACCAATATGT--GGACACCTATACCCAGCTTTTGGGCGCACCGAGATGG 510  
 QY 485 TACAAGTGGCTGGCTTTCAGCGAGGACTGTCTGTACCTGAACGTGTAGCGCGCGCGCGC 544  
 Db 511 AACCCCAACCGTGAGCTGAGCGAGGAGTCCCTGTACCTCAACGTGTGGACACCAATCCCC 570  
 QY 545 GCGCCCGGGGATCCCGAGCTGCCAGTGTGCTGTGTTTCCCGGAGGCGCTTTCATCGTG 604  
 Db 571 CGGCC--TACATCCCCACCCCTGCTCTGTCTGGATCTATGGGGTGGCTTCTACAGT 627  
 QY 605 GCGCTGTCTTTT-----CGTACAGGGCTCTGACTTGGCCGCCCGCGAGAAAGTGGTG 659  
 Db 628 GGGGCTCTCTCTTGGAGCTGTACGATGGCGCTCTTGTGTACAGGCGCGAGGAGCTGTG 687  
 QY 659 CTGGTGTCTTTCAGACACAGGCTCGGCATCTTTCGGCTTCTTGTAGCAGCAGCAGCAGCC-- 716  
 Db 688 CTGGTGTCTTCACTAAGTACCGGCTGGAGCTTTCGGCTTCTTGGCCCTTCCCGGGAGCGGA 747  
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 Db 748 GAGGCGCGGGCAATGTGGTCTCTCTGGATCAGAGGCTGGCCCTTGCAGTGGGTGACAGAG 807  
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Db 808 AACGTGGCAGCCTTCGGGGGTGACCCGACATCACTGACGCTGTTTGGGAGAGCGCGGGA 867  
Qy 836 GCCATGAGCATCTCAGGACTGATGTCACCCCTAGCCTCGGCTCTTCCATCGGCC 895  
Db 868 GCCCCTCGTGGGCATGCACTGCTGTCCCGCCAGCGGGGCCCTTCCACAGGGCC 927  
Qy 896 ATTTCCAGAGTGG-----CACCGCTTATTCAGACTTTTTCATCACTAGTACCCACTG 949  
Db 928 GTGCTGAGAGCGGTGCCCAATGACCTGGGCCACGCTGGGCATGGGAGAGGCCCGT 987  
Qy 950 AAAGTGGCCAGAGGTTGCCACCTGGCTGGATGCAACACACAGCAGCAGATCCTG 1009  
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Qy 1010 GTAAATGCTGAGGCACTATCAGGACCAAGGTGATGTGTGTCTCAACAAGATGAGA 1069  
Db 1048 GACACAGAGCTGTAGCTGCCITCGGACAGCAGCGCAGGTCTCTGGTGA----- 1100  
Qy 1070 TTCTCTCAACTGAACTTCAGAGAGACCCGGAAGATTAATCTGGTCCATGACCCCTGTG 1129  
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Qy 1130 GTGATGGTGTGGTGATCCAGATGACCTTTGGTGTCTCTGACCCAGGGAAGTTCA 1189  
Db 1159 GTAGTGGAGACTTCTCAGTACACCCAGAGGCCCTCATCAAGCGGAGACTTCCAC 1218  
Qy 1190 TCTGTGCCCTACCTTCTAGTGTCAACAACCTGGAATTCATTAATTTGCTTTCCTTATC 1249  
Db 1219 GGCCTGCAAGTGTGTGGTGTGCTCAAGGATCAGGGCTCGTATTCTGTGTTACGGG 1278  
Qy 1250 ATGAAGTTCGGCTAAACCGGAGCGATGAGAAAGGAACCATCACTAAGATGCTCTGG 1309  
Db 1279 GCCCAGGCTTCAACAAAGACAGAGTCTCTCATAGCCGGCGAGTCTCTGGCGGG 1338  
Qy 1310 AGTACCCGACCCCTGTTGAATATCAACAGGAGCAGGTACCACTTGTGTGGAGAGTAC 1369  
Db 1339 GTGCGGCTGGGGTTCGCCAGTAAAGTGAAGTGCAGCGAGGCTGTGGTCTGCTTAC 1398  
Qy 1370 CTGACAAATGATGAGTACTGGAAGATGCTACAAACCGTATGATGACATAGTT 1429  
Db 1399 ACAGCTGGTGTGATCCGAGGACCCGGCAGCGCTGAGGAGGCCCTTGACGATGTGGT 1458  
Qy 1430 CAAGATGCCACTTTCGTGTATGCCACACTGACAGACTGCTCACTACCACCGAGATGCCGC 1489  
Db 1459 GGGACCAATGTCGTGTGCCCGTGGCCAGCTGCTGGGAGCTGGCTGCCAGGT 1518  
Qy 1490 CTCCTGTCTACCTGTATGAATTTGAGCAGCAGCTCGTGGATATCGTCAACCCCGC 1549  
Db 1519 GCCCGGCTACGCTACGCTTTTGAACACCGTGC---TTCCAGCTCTCTCGGCCCTG 1575  
Qy 1550 ACTGATGGGCGAGACCATGGGATGAGATGATCTTCTTTGGGGGCCCTT---CGCC 1606  
Db 1576 TGGATGGGGTGCCCGCTACGAGATCGAGTTCATCTTTGGGATCCCGCTGGACCCC 1635  
Qy 1607 ACAGCCTTTCATGGGTAGGAGAGGCACTTAGCCTCCAGATGATGAATACTGGGC 1666  
Db 1636 TCTCGAAATACACGGCAGAGGAAATCTTCCAGGAGCTGATGCGATACCTAGGCT 1695  
Qy 1667 AACTTTCGCGCAGGGAACCCCAATGA 1695  
Db 1696 AACTTTCGCGCAGGGAATCCCAATGA 1724

RESULT 7  
US-08-370-156-1  
; Sequence 1, Application US/08370156  
; Patent No., 5932780  
; GENERAL INFORMATION:  
; APPLICANT: Soreq, Hermona  
; APPLICANT: Zakut, Haim  
; APPLICANT: Shani, Moshe  
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
; TITLE OF INVENTION: ANTICHOLINESTERASE SUBSTANCES

; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: Reising, Ethington, Barnard & Perry  
; STREET: P.O. Box 4390  
; CITY: Troy  
; STATE: Michigan  
; COUNTRY: US  
; ZIP: 48099  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/370,156  
; FILING DATE:  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kohn, Kenneth I.  
; REGISTRATION NUMBER: 30,955  
; REFERENCE/DOCKET NUMBER: P-307 (Mulford)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (810) 689-3500  
; TELEFAX: (810) 689-4071  
; INFORMATION FOR SEQ ID NO. 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2256 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; US-08-370-156-1

Query Match 7.5%; Score 148.2; DB 2; Length 2256;  
Best Local Similarity 48.3%; Pred. No. 1.4e-30;  
Matches 680; Conservative 0; Mismatches 693; Indels 36; Gaps 8;  
Qy 305 CCCATCCAAAGTCTTTTATAGGAGTCCCTTCTCCAGACCTCTCTAGGTATCTCTCAGGTTT 364  
Db 334 CTGTCTCTGCTTCTTCTGGGATCCCTTTGGGAGCCACCATGGGACCCCGTCTTT 393  
Qy 365 GCACTTCAGAAACCCCGAGCCCTTGGAAAGAAATCAGAGATGCTACCACTACCCGCT 424  
Db 394 CTGCCACCGGAGCCCAAGCAGCCTTGGTCAGGGGTGGTAGACGCTTCAACCTTCCAGAGT 453  
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Db 454 GTCTCTACCAATATGT---GGACACCTATACCCAGGTTTGGGGGACCGAGATGTGG 510  
Qy 485 TACAAGTGGCTGCGCTTCAGCGAGGACTGTCTGTACTGTAAACGTGTACGCGCCGCGCGC 544  
Db 511 AACCCCAACCGTGAGCTGAGCGAGGACTGCTGTACCTCAACGTGTGGACACCATACCCC 570  
Qy 545 GGGCCGGGGATCCCAAGTCCAGTCCAGTGTGTTCCCGGAGGCGCTTCATCGT 604  
Db 571 CGGCC---TACATCCCCACCCCTGCTCTGCTGGATCTATGGGGGTGGCTTCTACAGT 627  
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Qy 659 CTGGTGTCTTCAGCAGCAGCTCGGCTCTTCGGCTTCTCGGCTTCCTGAGCAGGAGAGGCC-- 716  
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Db 868 GCGGCTGGTGGGCAATGACCTGCTGCGCGCCAGCGGGGCTGTTCACAGGGCC 927
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QY 1310 AGTACCGCCACCTGTTGAATATCAACAGAGCAGGTACCACTTGTGTGGAGAGTAC 1369
Db 1339 GTGCGGGTGGGGTTCCCGAGTAAAGTACCTGCGACCCGAGGCTGTGGTCTGCTTAC 1398
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Db 1399 ACAGACTGGCTGCTATCCGAGGACCCGCGACCGCTGAGGAGGCGCTGAGCGATGGTG 1458
QY 1430 CAAGATGCACTTTCGCTGATGCCACACTGCGAGACTGCTCACTACCAACGAGATGCGGC 1489
Db 1459 GCGACCAATATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1518
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QY 1667 AACTTTGCGCCAGAGNAACCCCAATGA 1695
Db 1696 AACTTTGCGCCAGAGGGATCCCAATGA 1724

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RESULT 8  
 US-08-814-095-1  
 ; Sequence 1, Application US/08814095  
 ; Patent No. 6025183  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soreq, Hermona  
 ; APPLICANT: Zakut, Haim  
 ; APPLICANT: Shani, Moshe  
 ; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
 ; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: KOHN & ASSOCIATES

```

; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2256 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "ACHE gene comprising exons
; DESCRIPTION: 2, 3, 4 and 6"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-814-095-1

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Query Match 7.5%; Score 148.2; DB 3; Length 2256;
Best Local Similarity 48.3%; Pred. No. 1.4e-30;
Matches 680; Conservative 0; Mismatches 693; Indels 36; Gaps 8;

QY 305 CCATCCCAAGTCTTTTAGGAGTCCCTTCTCCAGACCTCTCTAGTATCTCTCAGGTTT 364
Db 334 CTGTCTCTGTTTCTCTGGGATCCCTTTCCGAGGACCCATGGAGCCCGTCTGCTTT 393
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Qy 1667 AACTTTGCGGCACAGGAAACCCCAATGA 1695  
Db 1696 AACTTTGCGGCACAGGAGATCCCAATGA 1724

RESULT 9

US-08-318-826A-7

; Sequence 7, Application US/08318826A

; Patent No. 5891725

; GENERAL INFORMATION:

; APPLICANT: Soreq, Hermona

; APPLICANT: Zakut, Haim

; APPLICANT: Eckstein, Fritz

; TITLE OF INVENTION: Synthetic Antisense

; TITLE OF INVENTION: Oligodeoxynucleotides and Pharmaceutical Compositions

; CONTAINING THEM

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kohn & Associates

; STREET: 30500 No. 5891725thwestern Hwy., Suite 410

; CITY: Farmington Hills

; STATE: Michigan

; COUNTRY: US

; ZIP: 48334

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/318,826A

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Kohn, Kenneth I.

; REGISTRATION NUMBER: 30,955

; REFERENCE/DOCKET NUMBER: 2391.00001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (248) 539-5050

; TELEFAX: (248) 539-5055

; INFORMATION FOR SEQ ID NO: 7:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3016 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA to mRNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 160..2010

; OTHER INFORMATION: /note= "Splice Variant: Exons 1, 2,

; OTHER INFORMATION: 3, 4, 5 and 6"

US-08-318-826A-7

Query Match 7.5%; Score 148.2; DB 2; Length 3016;

Best Local Similarity 48.3%; Pred. No. 1.6e-30;

Matches 680; Conservative 0; Mismatches 693; Indels 36; Gaps 8;

Qy 305 CCCATCCAGTCTTTTAGGAGTCCCTTCTCCAGACCTCTCTAGGTATCTCAGGTTT 364

Db 334 CTGTCTCTGCTTCTCTGGCATCCCTTTGGGAGCCACCCATGGGACCCCGTCTT 393

Qy 365 GCACCTCCAGAACCCCGAGCCCTGGAAAGAAATCAGAGATGCTACCACTACCCGCT 424

Db 394 CTGCCACCGAGCCCAAGCAGCTTTGGTCAGGGGTGGTAGCGCTACAACTTCCAGAGT 453

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 1636 TCTGAAACTACAGGAGGAGAAATCTTCGCCAGGACTGATGCACTACTGGCC 1695  
 1667 AACTTTGCCGACAGGAAACCCCAATGA 1695  
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US-08-370-156-5  
 ; Sequence 5, Application US/08370156  
 ; Patent No. 5932780  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soreq, Hermona  
 ; APPLICANT: Zakut, Haim  
 ; APPLICANT: Shani, Moshe  
 ; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
 ; TITLE OF INVENTION: ANTICHLINESTERASE SUBSTANCES  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Reising, Ethington, Barnard & Perry  
 ; STREET: P.O. Box 4390  
 ; CITY: Troy  
 ; STATE: Michigan  
 ; COUNTRY: US  
 ; ZIP: 48099  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/370,156  
 ; FILING DATE:  
 ; CLASSIFICATION: 536  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Kohn, Kenneth I.  
 ; REGISTRATION NUMBER: 30,955  
 ; REFERENCE/DOCKET NUMBER: P-307 (Multford)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (810) 689-3500  
 ; TELEFAX: (810) 689-4071  
 ; INFORMATION FOR SEQ ID NO: 5:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 3016 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: 160..2010  
 ;  
 US-08-370-156-5

Query Match 7.5%; Score 148.2; DB 2; Length 3016;  
 Best Local Similarity 48.3%; Pred. No. 1.6e-30;  
 Matches 680; Conservative 0; Mismatches 693; Indels 36; Gaps 8;  
 QY 305 CCCATCCAAAGTCTTTTAGGAGTCCCTTCTCCAGAGCTCCTCTAGGTATCCTCAGGTTT 364  
 DB 334 CTTGTCTCTGCTTTCTTGGGCATCCCTTTGCGGAGCCACCCATGGGACCCCGTCGCTTT 393  
 QY 365 GCACCTCAGAACCCCGGAGCCCTGGAAAGGATCAGAGATGCTACCACTACCCGCT 424  
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 DB 454 GTCTGTACCAATATGT---GGACACCTATACCCAGGTTTGGGAGCACCAGATGTGG 510  
 QY 485 TACAAGTGGTGGCTTCAGCGAGGACTGTCTGTACTGAACTGTACGCGCGCGCGCCGC 544  
 DB 511 AACCCCAACCGTGAAGTGAAGGAGGCTGCTGTACCTCAACGCTGTGGACACCATACCCC 570  
 QY 545 GCGCCCGGGATCCCGAGTCCAGCTGCCAGTGTGGTCTGGTTCGCGGAGGCGCTTCATCGTG 604  
 DB 571 CGGCC---TACATCCCCACCCCTGTCTCTGTGGATCTATGGGGTGGCTTCTACAGT 627  
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[illegible]

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US-08-814-095-5
; Sequence 5, Application US/08914095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/POCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3016 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Alternatively spliced AChE
; DESCRIPTION: comprising exons 2, 3, 4, 5 and 6"
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 160..2010
US-08-814-095-5

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	Query Match	7.5%;	Score 148.2;	DB 3;	Length 3016;
	Best Local Similarity	48.3%;	Pred. No. 1.6e-30;		
	Matches 680;	Conservative 0;	Mismatches 693;	Indels 36;	Gaps 8;
QY	305	CCCATCCAAGTC	TTTTAGGAGTCC	CTTCTCAGAGCT	CTCTFAGTATCCTCAGAGTTT 364
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QY 1370 CTGACAAATGTAATGAGTACCTGGAAGTGTCTAGAAACCGTATGATGACATAGTT 1429  
DB 1399 ACAGACTGGTGTGATCCCGAGGACCGGACGCTTGGAGGAGGCTTGGAGATGTGGT 1458  
QY 1430 CAGATGCACTTGTGTATGCCACACTGCACTGCACTTACACGAGATGCGCGC 1489  
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DB 1519 GCGCGGTCTACGCTACGCTTTGAACACCGTGC---TTCCAGCGCTCTCTGGGCCCTG 1575  
QY 1550 ACTGATGGGGCAGACCATGGGATGAGATGTACTTCTCTTTGGGGGCGCCCTT---CGCC 1606

DB 1576 TGGATGGGGTGGCCCGACGGCTACGAGATCGAGTTTCATCTTTGGGATCCCGCTGGACCC 1635  
QY 1607 ACAGGCTTTCATGGGTAAAGGAGAGGCACTTAGCTTCCAGATGATGAATAACTGGGCC 1666  
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QY 1667 AACTTTGGCCGACAGGAAACCCCAATCA 1695  
DB 1696 AACTTTGGCCGACAGGAGATCCCAATCA 1724

## RESULT 14

US-08-814-095-3  
; Sequence 3, Application US/08814095  
; Patent No. 6025183  
; GENERAL INFORMATION:  
; APPLICANT: Soreq, Hermona  
; APPLICANT: Zakut, Haim  
; APPLICANT: Shani, Moshe  
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KOHN & ASSOCIATES  
; STREET: 30500 No. 6025183thwestern Highway, Suite 410  
; CITY: Farmington Hills  
; STATE: Michigan  
; COUNTRY: U.S.  
; ZIP: 48334  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/814,095  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Montgomery, Ilene N.  
; REGISTRATION NUMBER: 38,972  
; REFERENCE/DOCKET NUMBER: 2391.00066  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (248) 539-5050  
; TELEFAX: (248) 539-5055  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3096 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; DESCRIPTION: /desc = "alternatively spliced AchE  
; DESCRIPTION: comprising exons 2, 3, 4 and 5 as well as the translated portion  
; DESCRIPTION: of Intron 4 (readthrough)"  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 160..1959  
US-08-814-095-3

Query Match 7.5%; Score 148.2; DB 3; Length 3096;  
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RESULT 15

US-08-814-095-7  
; Sequence 7, Application US/08814095  
; Patent No. 6025183  
; GENERAL INFORMATION:  
; APPLICANT: Sored, Hermona  
; APPLICANT: Zakut, Haim  
; APPLICANT: Shani, Moshe  
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR  
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: KOHN & ASSOCIATES  
; STREET: 30500 No. 6025183thwestern Highway, Suite 410  
; CITY: Farmington Hills  
; STATE: Michigan  
; COUNTRY: U.S.  
; ZIP: 48334  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/814,095  
; FILING DATE:  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Montgomery, Ilene N.  
; REGISTRATION NUMBER: 38,972  
; REFERENCE/DOCKET NUMBER: 2391.00066  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (248) 539-5050  
; TELEFAX: (248) 539-5055  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 35060 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
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; DESCRIPTION: promotor, ACHE gene and ARS gene"  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
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; ORGANISM: Homo sapiens  
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; CHROMOSOME/SEGMENT: 7q22  
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Best Local Similarity 56.0%; Pred. No. 5.5e-27; Matches 347; Conservative 0; Mismatches 258; Indels 15; Gaps 4;

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Qy 365 GCACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGAGATGCTACCACTTACCGCCT 424
Db 24344 CTGCCACCGGAGCCCAAGCAGCCTTGGTCAGGGGTGGTAGACGCTACAACTTCCAGAGT 24403
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Db 24461 AACCCCAACCGTGAGCTGACGAGGACTGCTGTACTCAACGTGTGGACACCATACCCC 24520  
Qy 545 GCGCCCGGGGATCCCCAGCTGCCAGATGAGTCTGTGTTCCGGGAGGCGCTTTCATCGTG 504  
Db 24521 CGGCC--TACATCCCCCACCCTGTCTCTGTGGATCTATGGGGGTGGCTTCTACAGT 24577  
Qy 605 GCGCTGCTTCTT-----CGTACGAGGGCTCTGACTTGGCCGCCCGCGAGAAAGTGTG 658  
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Qy 776 AACATCGAGCCTTCGGGGGAGACCCAGGAAATGTGACCTGTTCGGCCAGTCGCGGGG 835  
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Qy 836 GCCATGAGCATCTCAGGACTGATGATGTACCCCTAGCCTCGGGTCTCTTCCATCGGGC 895  
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Qy 896 ATTTCCAGAGTGCACCGC 915  
Db 24878 GTGCTGAGAGCGGTGCCCC 24897

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Job time : 174.88 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 15:30:03 ; Search time 898.854 Seconds  
(without alignments)  
10824.678 Million cell updates/sec

Title: US-10-001-227-1

Perfect score: 1983

Sequence: 1 ccttagccaattcgccga.....gtttaacctgcaggactag 1983

Scoring table: IDENTITY NJC

Gapop 10.0 , Gapext 1.0

Searched: 3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters: 6451454

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	1752	88.4	1752	15	US-10-001-227-3
4	1459.4	73.6	2178	16	US-10-108-260A-339
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#### ALIGNMENTS

RESULT 1

US-10-001-227-1

; Sequence 1, Application US/10001227

; Publication No. US20030166900A1

; GENERAL INFORMATION:

; APPLICANT: KAPPELLER-LIBERMANN

; APPLICANT: SILOS-SANTIAGO

; TITLE OF INVENTION: METHODS OF USING 18903 TO TREAT PAIN AND

; TITLE OF INVENTION: PAIN-RELATED DISORDERS

; FILE REFERENCE: MNI-199

; CURRENT APPLICATION NUMBER: US/1001,227

; CURRENT FILING DATE: 2001-11-30

; PRIOR APPLICATION NUMBER: 60/250929

; PRIOR FILING DATE: 2000-11-30

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 1983

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (98)....(1849)

US-10-001-227-1

Query Match 100.0%; Score 1983; DB 15; Length 1983;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1983; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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301 GACACCCATCAAGTCTTTTAGAGTCCCTCTCCAGACCTCTCTAGGTATCTCTCAG 360  
301 GACACCCATCAAGTCTTTTAGAGTCCCTCTCCAGACCTCTCTAGGTATCTCTCAG 360  
361 GTTTGCACTCCAGAACCCCGAGCTTGGAAAGGAATCAGAGATGCTACCACTACCC 420  
361 GTTTGCACTCCAGAACCCCGAGCTTGGAAAGGAATCAGAGATGCTACCACTACCC 420  
421 GCCTGGGTGCTGAGAGTCTTGGGCGCAGCTGGCTCGATGATGATGATGATGATGATGAT 480  
421 GCCTGGGTGCTGAGAGTCTTGGGCGCAGCTGGCTCGATGATGATGATGATGATGATGAT 480  
481 ACGGTACAAAGTGGTGGCTTTCAGCGAGGAGCTGTCTGTACCTGAAACGTGTACGCGCGG 540  
481 ACGGTACAAAGTGGTGGCTTTCAGCGAGGAGCTGTCTGTACCTGAAACGTGTACGCGCGG 540  
541 GCGGCGCGCGGGATCCCAAGCTGCGAGTGTGCTGTGCTGAAACGTGTACGCGCGGCTTCAT 600  
541 GCGGCGCGCGGGATCCCAAGCTGCGAGTGTGCTGTGCTGAAACGTGTACGCGCGGCTTCAT 600  
601 CGTGGGCGCTCTCTTCTGACAGAGGCTCTGACTTGGCGCGCGCGAGAAAGTGTGTCT 660  
601 CGTGGGCGCTCTCTTCTGACAGAGGCTCTGACTTGGCGCGCGCGAGAAAGTGTGTCT 660  
661 GGTGTTCTGAGCAGCAGGCTTGGCTTCTGGCTTCTGAGCAGCAGCAGCAGCAGCAGCAGC 720  
661 GGTGTTCTGAGCAGCAGGCTTGGCTTCTGGCTTCTGAGCAGCAGCAGCAGCAGCAGCAGC 720  
721 GCGGGGAACTGGGGGCTGCTGGAACAGATGGGGCTCTGCTGCTGGCTGGCTGAGAGAACAT 780  
721 GCGGGGAACTGGGGGCTGCTGGAACAGATGGGGCTCTGCTGCTGGCTGGCTGAGAGAACAT 780  
781 GCGAGCTTGGGGGAGACCCAGAAATGTGACCTGTTGGCCAGTGGCGGGGGCCAT 840  
781 GCGAGCTTGGGGGAGACCCAGAAATGTGACCTGTTGGCCAGTGGCGGGGGCCAT 840  
841 GAGCATCTCAGGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
841 GAGCATCTCAGGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900  
901 CCAGAGTGGCACCGCTTATTCAGACTTTTCATCAGTGTAAACCCACTGAAAGTGGCCAA 960  
901 CCAGAGTGGCACCGCTTATTCAGACTTTTCATCAGTGTAAACCCACTGAAAGTGGCCAA 960  
961 GAAAGTGGCCACCTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020  
961 GAAAGTGGCCACCTGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020  
1021 GAGGCACTATCAGGACCAAGGTGATGCTGTGTGTCACCAAGATGATGATGATGATGATGAT 1080  
1021 GAGGCACTATCAGGACCAAGGTGATGCTGTGTGTCACCAAGATGATGATGATGATGATGAT 1080  
1081 GAACTTCAGAGACCCGGAAGAGATATCTGCTGATGATGATGATGATGATGATGATGATGAT 1140  
1081 GAACTTCAGAGACCCGGAAGAGATATCTGCTGATGATGATGATGATGATGATGATGATGAT 1140  
1141 GGTGATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200  
1141 GGTGATCCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200  
1201 CCTTCTAGGTGTCAACCAACTGGGAATCAATTTGGCTCTTCCCTTATATCAATGAAGTTCC 1260

1201 CTTCTAGGTGTCAACCACTGGAAATCAATTTGGCTTTGGCTTTATATCATGAAGTTCCC 1260  
1261 GCTAAACCGGAGCGATGAGAAAGAAACCATCACTAAGATGCTTGGAGTACCCGAC 1320  
1261 GCTAAACCGGAGCGATGAGAAAGAAACCATCACTAAGATGCTTGGAGTACCCGAC 1320  
1321 CTTGTGATATATCAACAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
1321 CTTGTGATATATCAACAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380  
1381 CAATGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
1381 CAATGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440  
1441 TTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500  
1441 TTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500  
1501 CTTGTATCAATTTGAGCAGCAGCTGCTGGAATTAATCGTCAAAACCCGCACTGATGGGC 1560  
1501 CTTGTATCAATTTGAGCAGCAGCTGCTGGAATTAATCGTCAAAACCCGCACTGATGGGC 1560  
1561 AGACCATGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
1561 AGACCATGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620  
1621 GGGTAAGGAGAGGACCTTACCTCCAGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
1621 GGGTAAGGAGAGGACCTTACCTCCAGATGATGATGATGATGATGATGATGATGATGATGAT 1680  
1681 AGGAAACCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
1681 AGGAAACCCCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1740  
1741 CTTGAGTGTGATTTTACCAAGAGTGGGATGATGATGATGATGATGATGATGATGATGATGAT 1800  
1741 CTTGAGTGTGATTTTACCAAGAGTGGGATGATGATGATGATGATGATGATGATGATGATGAT 1800  
1801 TTGAT 1860  
1801 TTGAT 1860  
1861 ATGAGGAGAGAGCAAG 1920  
1861 ATGAGGAGAGAGCAAG 1920  
1921 ATGAGCATACCTGGGAGCAAGAGATTTACCAAGGAGGAAATTCGTTTAAACCTTCAGGAC 1980  
1921 ATGAGCATACCTGGGAGCAAGAGATTTACCAAGGAGGAAATTCGTTTAAACCTTCAGGAC 1980  
1981 TAG 1983  
1981 TAG 1983

## RESULT 2

US-10-343-593-29  
; Sequence 29, Application US/10343593  
; Publication No. US20040110259A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.; BAUGHN, Mariah R.;  
; APPLICANT: BRUNS, Christopher M.; DAS, Debopriya;  
; APPLICANT: DELBEANE, Angelo M.; DING, Li;  
; APPLICANT: ELIOT, Vicki S.; GANDHI, Ameena R.;  
; APPLICANT: GRIFFIN, Jennifer A.; HAPALIA, April J.A.;  
; APPLICANT: KHAN, Farrah A.; LAL, Preeti G.;  
; APPLICANT: LEE, Sally; LU, Dying Aina M.;  
; APPLICANT: LU, Yan; ARVIZU, Chandra S.;  
; APPLICANT: RAMKUMAR, Jayalaxmi; RING, Huijun Z.;  
; APPLICANT: SANTANWALA, Madhusudan M.; TANG, Y. Tom;  
; APPLICANT: THANGAVELU, Kavitha; THORNTON, Michael;  
; APPLICANT: TRIBOULEY, Catherine M.; CHAWLA, Narinder K.;

APPLICANT: WARREN, Bridget A.; YANG, Junming;  
APPLICANT: YAO, Monique G.; YUE, Henry  
TITLE OF INVENTION: DRUG METABOLIZING ENZYMES  
FILE REFERENCE: PI-0185 USN  
CURRENT APPLICATION NUMBER: US/10/343,593  
CURRENT FILING DATE: 2003-01-29  
PRIOR APPLICATION NUMBER: US 60/223,055  
PRIOR FILING DATE: 2000-08-04  
PRIOR APPLICATION NUMBER: US 60/224,728  
PRIOR FILING DATE: 2000-08-11  
PRIOR APPLICATION NUMBER: US 60/226,440  
2000-08-18  
PRIOR APPLICATION NUMBER: US 60/228,067  
PRIOR FILING DATE: 2000-08-24  
PRIOR APPLICATION NUMBER: US 60/230,063  
PRIOR FILING DATE: 2000-08-31  
PRIOR APPLICATION NUMBER: US 60/232,244  
PRIOR FILING DATE: 2000-09-13  
PRIOR APPLICATION NUMBER: US 60/234,269  
PRIOR FILING DATE: 2000-09-20  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: PERL Program  
SEQ ID NO 29  
LENGTH: 2081  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No: 7478588CB1  
US-10-343-593-29

Query Match 97.3%; Score 1928.6; DB 17; Length 2081;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1931; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	18	CGAGGCTCCGCCAGTACTTGTGCGCAGGAGTAAGAGCAGATAAAGTGTCTCAC	77
Db	27	CAATCCCCCGCCAGTACTTGTGCGCAGGAGTAAGAGCAGATAAAGTGTCTCAC	86
Qy	78	ACACTGTAGACAGCGCTACCATGCCACAGTGTGCCATCCACAGTGTGCCATCAC	137
Db	87	ACACTGTAGACAGCGCTACCATGCCATCCACAGTGTGCCATCCACAGTGTGCCATCAC	146
Qy	138	TCCTGCCCCACAGCAGGAGCTGGTGGAGCATGAGTGGATTCTGTGCTGGAGCCTCACCC	197
Db	147	TCCTGCCCCACAGCAGGAGCTGGTGGAGCATGAGTGGATTCTGTGCTGGAGCCTCACCC	206
Qy	198	TCTGCTGTGGCGCAGACGCGCTTGGTGGCTTGCATCCACAGAGCGCTCAAGTGTCA	257
Db	207	TCTGCTGTGGCGCAGACGCGCTTGGTGGCTTGCATCCACAGAGCGCTCAAGTGTCA	266
Qy	258	CCAAATATGGAACCTCTCAGGAAACAGATGATGTGGGGAAGACACACCCATCCAACTCT	317
Db	267	CCAAATATGGAACCTCTCAGGAAACAGATGATGTGGGGAAGACACACCCATCCAACTCT	326
Qy	318	TTTTAGAGTCCCTTCTCCAGACCTCTCTAGGTATCTCTAGGTTTGCACCTCCAGAAC	377
Db	327	TTTTAGAGTCCCTTCTCCAGACCTCTCTAGGTATCTCTAGGTTTGCACCTCCAGAAC	386
Qy	378	CCCGGAGCCTCGGAAGGATCAGATGCTACCACTACCGCCTGGGTGCTGCAGG	437
Db	397	CCCGGAGCCTCGGAAGGATCAGATGCTACCACTACCGCCTGGGTGCTGCAGG	446
Qy	438	AGTCTGGGGCAGCTGGCTCGATGATCGTCAGATGTCAGCAGCGGGAAACGATGAGTGGCTGC	497
Db	447	AGTCTGGGGCAGCTGGCTCGATGATCGTCAGATGTCAGCAGCGGGAAACGATGAGTGGCTGC	506
Qy	498	GCTTCAGGAGGACTGTCTGTACCTGACGTGACGCGCGCGCGCGCGCGCGCGCGGATC	557
Db	507	GCTTCAGGAGGACTGTCTGTACCTGACGTGACGCGCGCGCGCGCGCGCGCGCGGATC	566
Qy	558	CCCAGCTCCAGTGTGTGTGTCCGGGAGGCGCTTCATCTGTGGGCGCTGCTTCTT	617

Db	567	CCCAGCTCCAGTGTGTGTGTCCGGGAGGCGCTTCATCTGTGGGCGCTGCTTCTT	626
Qy	618	CGTACGAGGCTCTGACTTGGCCCGCCGAGAAAGTGGTGTCTGTGTCTGTCTGAGCACA	677
Db	627	CGTACGAGGCTCTGACTTGGCCCGCCGAGAAAGTGGTGTCTGTGTCTGTCTGAGCACA	686
Qy	678	GGCTCGGCATCTCGGCTTCTGAGCAGGAGCAGCAGCAGCGCGCGGGAACTGGGGGC	737
Db	687	GGCTCGGCATCTCTCGGCTTCTGAGCAGGAGCAGCAGCAGCGCGCGGGAACTGGGGGC	746
Qy	738	TGCTGGACAGATGGCGCTCTCGGCTGGGTGTCAGGAGAAACATCGACGCTTCGGGGGAG	797
Db	747	TGCTGGACAGATGGCGCTCTCGGCTGGGTGTCAGGAGAAACATCGACGCTTCGGGGGAG	806
Qy	798	ACCCAGGAATGTGACCTGTTCGGCAGTGGCGGGGGCCATGAGCATCTCAGACTGA	857
Db	807	ACCCAGGAATGTGACCTGTTCGGCAGTGGCGGGGGCCATGAGCATCTCAGACTGA	866
Qy	858	TGATGTCACTCCCTAGCCTCGGCTCTCTTCCATCGGGGCCATTTCCAGAGTGGCACCCTG	917
Db	867	TGATGTCACTCCCTAGCCTCGGCTCTCTTCCATCGGGGCCATTTCCAGAGTGGCACCCTG	926
Qy	918	TATTGAGCTTTTCACTAGTAACCCACTGAAAGTGGCCAAAGTTCGCCACCTGG	977
Db	927	TATTGAGCTTTTCACTAGTAACCCACTGAAAGTGGCCAAAGTTCGCCACCTGG	986
Qy	978	CTGGATGCAACCAACACAGCAGATCTCTGTAACCTGCTGAGGCACTATCAGGGA	1037
Db	987	CTGGATGCAACCAACACAGCAGATCTCTGTAACCTGCTGAGGCACTATCAGGGA	1046
Qy	1038	CCAAGTGTGCTGTGTCCAAAGATGAGATCTCTCAACTGAACTTCCAGAGAGACC	1097
Db	1047	CCAAGTGTGCTGTGTCCAAAGATGAGATCTCTCAACTGAACTTCCAGAGAGACC	1106
Qy	1098	CGGAGAGATTTCTGGTCCATGAGCCCTGTGGTGGATGGTGTGATCCAGATGACC	1157
Db	1107	CGGAGAGATTTCTGGTCCATGAGCCCTGTGGTGGATGGTGTGATCCAGATGACC	1166
Qy	1158	CTTTGCTGTCTCTGACCCAGGAGGTTTTCATCTGTGCTCTCTCTAGTGTCAACA	1217
Db	1167	CTTTGCTGTCTCTGACCCAGGAGGTTTTCATCTGTGCTCTCTCTAGTGTCAACA	1226
Qy	1218	ACTCGAATTCATTTGGCTCTTGCCTTATATCATGAGTTCCCGTCAACCGGAGGGA	1277
Db	1227	ACTCGAATTCATTTGGCTCTTGCCTTATATCATGAGTTCCCGTCAACCGGAGGGA	1286
Qy	1278	TGAGAAAGGAAACCATCACTAAGATCTCTGAGTACCCGACCCCTGTGTAATATCAACA	1337
Db	1287	TGAGAAAGGAAACCATCACTAAGATCTCTGAGTACCCGACCCCTGTGTAATATCAACA	1346
Qy	1338	AGGAGAGGTACCACTTGTGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGA	1397
Db	1347	AGGAGAGGTACCACTTGTGTGGAGGAGTACCTGGACAATGTCAATGAGCATGACTGA	1406
Qy	1398	AGATGCTAGAAACCGTATGATGAGATGCTCAAGATGCCACTTTCGTGTATGCCACAC	1457
Db	1407	AGATGCTAGAAACCGTATGATGAGATGCTCAAGATGCCACTTTCGTGTATGCCACAC	1466
Qy	1458	TGCAGACTGCTCACTACCAAGATGCCGCTCCCTGTCTACCTGTATGAAATTTGAGC	1517
Db	1467	TGCAGACTGCTCACTACCAAGATGCCGCTCCCTGTCTACCTGTATGAAATTTGAGC	1526
Qy	1518	ACACGCTGTGGAATATCGTCAAAACCCGACCTGATGGGCGACACCATGGGGATGAGA	1577
Db	1527	ACACGCTGTGGAATATCGTCAAAACCCGACCTGATGGGCGACACCATGGGGATGAGA	1586
Qy	1578	TGTACTTCTCTTTGGGGGCCCTTTCGCCACAGGCTTTTCCATGGGTAAAGGAGGAC	1637
Db	1587	TGTACTTCTCTTTGGGGGCCCTTTCGCCACAGGCTTTTCCATGGGTAAAGGAGGAC	1646
Qy	1638	TTAGCCTCCAGATGATGAAATATCTGGGCCAACTTTGCCGACAGGAAACCCCATGATG	1697
Db	1647	TTAGCCTCCAGATGATGAAATATCTGGGCCAACTTTGCCGACAGGAAACCCCATGATG	1706



QY 1538 GTCAACCCCGCACTGATGGGCGAGACCATGGGGATGAGATGACTTCTCTTTGGGGC 1597  
D 1441 GTCAACCCCGCACTGATGGGCGAGACCATGGGGATGAGATGACTTCTCTTTGGGGC 1500  
QY 1598 CCCTTCCGCCACAGGCTTTCCATGGGTAAAGGAGAGGCACTTAGCCTCCAGATGATGAAA 1657  
D 1501 CCCTTCCGCCACAGGCTTTCCATGGGTAAAGGAGAGGCACTTAGCCTCCAGATGATGAAA 1560  
QY 1658 TACTGGGCCCACTTTGCCCGCACAGGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCA 1717  
D 1561 TACTGGGCCCACTTTGCCCGCACAGGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCA 1620  
QY 1718 CGCTACAAAGAGTAAAGTACCTGCAGCTGGATTTTACCAAGAGTGGGCATGAAG 1777  
D 1621 CGCTACAAAGAGTAAAGTACCTGCAGCTGGATTTTACCAAGAGTGGGCATGAAG 1680  
QY 1778 CTCAGGAGAGAGATGGCTTTTGGATGAGTCTGTACAGTCTCAAGACCTGAGAAG 1837  
D 1681 CTCAGGAGAGAGATGGCTTTTGGATGAGTCTGTACAGTCTCAAGACCTGAGAAG 1740  
QY 1838 CAGAGGCAATTC 1849  
D 1741 CAGAGGCAATTC 1752

## RESULT 4

US-10-108-260A-339  
; Sequence 339, Application US/10108260A  
; Publication No. US20040005560A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20040005560A1 full length cDNA  
; FILE REFERENCE: HI-A0106  
; CURRENT APPLICATION NUMBER: US/10/108,260A  
; CURRENT FILING DATE: 2002-03-27  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 339  
; LENGTH: 2178  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-108-260A-339

Query Match 73.6%; Score 1459.4; DB 16; Length 2178;

Best Local Similarity 96.4%; Pred. No. 0;  
Matches 1526; Conservative 0; Mismatches 1; Indels 56; Gaps 1;

QY 426 GGTGCTGCAGAGTCTCTGGGCGCAGCTGGGCTCGATGTACGTACGACGCGGAAACGGT 485  
D 86 GGTGCTGCAGAGTCTCTGGGCGCAGCTGGGCTCGATGTACGTACGACGCGGAAACGGT 145  
QY 486 ACAAGTGGCTGCGCTTCAGGAGGACTGTCTGTACCTGAACTGTAACGCGCGCGCG 545  
D 146 ACAAGTGGCTGCGCTTCAGGAGGACTGTCTGTACCTGAACTGTAACGCGCGCGCGCG 205  
QY 546 CGCCGGGGATCCCGAGCTGCTGATGCTGGTCCCGGGAGGCGCTTCATCGTGG 605  
D 206 CGCCGGGGATCCCGAGCTGCTGATGCTGGTCCCGGGAGGCGCTTCATCGTGG 265  
QY 606 CGCTGCTTCTCGTACAGGGCTCTGACTTTGGCGCCCGCGAGAAAGTGTGCTGTGT 665  
D 266 CGCTGCTTCTCGTACAGGGCTCTGACTTTGGCGCCCGCGAGAAAGTGTGCTGTGT 325  
QY 666 TTCTGCAGCAGAGTGGGATCTTCGGCTTCCTGA----- 701  
D 326 TTCTGCAGCAGAGTGGGATCTTCGGCTTCCTGAAGGTGGCGGGGCGGTATCCCTTTGG 385  
QY 702 -----GCACGAGCAGACGCGCACGCGCGCGGAA 729  
D 386 GACCGCAGCTGTGCCACAGCGCGGAGCTGGCACGACGACGACGCGCGCGGAA 445  
QY 730 CTGGGGGCTGTGACCAAGATGGGCGCTCTCGCTGGGTGACGAGAACATCGCAGCCTT 789

D 446 CTGGGGGCTGCTGGACAGATGGGCGCTCTGGCGTGGGTGAGGAGAACATCGCAGCCTT 505  
QY 790 CGGGGAGACCCAGGAAATGTACCCCTGTTCGGCCAGTTCGGCGGGGCGCATGAGCATCTC 849  
D 506 CGGGGAGACCCAGGAAATGTACCCCTGTTCGGCCAGTTCGGCGGGGCGCATGAGCATCTC 565  
QY 850 AGGACTGATGATGTACCCCTTAGCTGGGTCTCTTCATCGGGCCATTTTCCAGAGTGG 909  
D 566 AGGACTGATGATGTACCCCTTAGCTGGGTCTCTTCATCGGGCCATTTTCCAGAGTGG 625  
QY 910 CACCGCTTATTCAGACTTTTTCATCACTAGTAAACCACTGAAAGTGGCCAGAGAGTGGC 969  
D 626 CACCGCTTATTCAGACTTTTTCATCACTAGTAAACCACTGAAAGTGGCCAGAGAGTGGC 685  
QY 970 CCACCTGCTGATGTCACCAACCAACAGACACAGATCTCGTAACTCGCTGAGGGCACT 1029  
D 686 CCACCTGCTGATGTCACCAACCAACAGACACAGATCTCGTAACTCGCTGAGGGCACT 745  
QY 1030 ATCAGGACCAAGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1089  
D 746 ATCAGGACCAAGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 805  
QY 1090 GAGAGCCCGGAGAGATTTCTGTCATGAGCCCTGTGTCGTCGTCGTCGTCGTCGTCGTC 1149  
D 806 GAGAGCCCGGAGAGATTTCTGTCATGAGCCCTGTGTCGTCGTCGTCGTCGTCGTCGTC 865  
QY 1150 AGATGACCTTTGTCCTCTGACCCAGGGGAAAGTTCATCTGTGTCGTCGTCGTCGTCGTC 1209  
D 866 AGATGACCTTTGTCCTCTGACCCAGGGGAAAGTTCATCTGTGTCGTCGTCGTCGTCGTC 925  
QY 1210 TGTCAACCACTGGAAATTCATTTGGCTTTCCTTATATCATGAGTTCGCGCTAAACCG 1269  
D 926 TGTCAACCACTGGAAATTCATTTGGCTTTCCTTATATCATGAGTTCGCGCTAAACCG 985  
QY 1270 GCAGGCGATGAGAAAGAAACCATCACTAAGATGCTCTGGAGTACCCGACCCCTGTTGAA 1329  
D 986 GCAGGCGATGAGAAAGAAACCATCACTAAGATGCTCTGGAGTACCCGACCCCTGTTGAA 1045  
QY 1330 TATCACCAGAGAGGATGACCACTTGTGTCGAGAGTACCTGGAATGTCATGAGCA 1389  
D 1046 TATCACCAGAGAGGATGACCACTTGTGTCGAGAGTACCTGGAATGTCATGAGCA 1105  
QY 1390 TCAGCTGGAAGATGCTACGAAACCGTATGATGACATAGTTCGAGATGTCCTGCTGTA 1449  
D 1106 TCAGCTGGAAGATGCTACGAAACCGTATGATGACATAGTTCGAGATGTCCTGCTGTA 1165  
QY 1450 TGCCCACTGACAGTCTCACTACCAACCGAGATGTCGCGCTTCTGCTGCTGATGA 1509  
D 1166 TGCCCACTGACAGTCTCACTACCAACCGAGATGTCGCGCTTCTGCTGCTGATGA 1225  
QY 1510 ATTTGAGCACCACGCTCGTGGAAATTCGTCAAAACCCGCACTGATGGGCGAGACATGG 1569  
D 1226 ATTTGAGCACCACGCTCGTGGAAATTCGTCAAAACCCGCACTGATGGGCGAGACATGG 1285  
QY 1570 GGATGAGATGACTTCTCTTTGGGGGCGCTTCGCCACAGGCTTCATGGGTAAAGGA 1629  
D 1286 GGATGAGATGACTTCTCTTTGGGGGCGCTTCGCCACAGGCTTCATGGGTAAAGGA 1345  
QY 1630 GAAGGCACTTAGCTTCAGATGATGAAATGCTGGGCGCACTTTCGCCGACAGGAAACCC 1689  
D 1346 GAAGGCACTTAGCTTCAGATGATGAAATGCTGGGCGCACTTTCGCCGACAGGAAACCC 1405  
QY 1690 CAATGATGGGAATCTGCGCTGTCGCGCACTGTCACCAAGGATGAAAGTACCTGAGCT 1749  
D 1406 CAATGATGGGAATCTGCGCTGTCGCGCACTGTCACCAAGGATGAAAGTACCTGAGCT 1465  
QY 1750 GAATTTTACCAAGAGTGGGATGAGCTCAAGGAGAGAGATGCTGCTTTTGTGATGAG 1809  
D 1466 GAATTTTACCAAGAGTGGGATGAGCTCAAGGAGAGAGATGCTGCTTTTGTGATGAG 1525  
QY 1810 TCTGTACAGTCTCAAGACCTGAGAGCAGAGCAATTTCTAAGGGTGGCTATGAGGAA 1869



Query Match	Best Local Similarity	Matches 1446;	Conservative	0;	Mismatches	0;	Indels	403;	Gaps	3;
224	GGTGCCTTGCACACCAAGAGGCTCAAGTGGTCCACCAATATGACCAAGCCCTGCAAGGAAA	283								
	Prior Application Number: 60/082796									
	Prior Filing Date: 1998-04-23									
	Prior Application Number: 60/083336									
	Prior Filing Date: 1998-04-27									
	Prior Application Number: 60/083322									
	Prior Filing Date: 1998-04-28									
	Prior Application Number: 60/083392									
	Prior Filing Date: 1998-04-29									
	Prior Application Number: 60/083495									
	Prior Filing Date: 1998-04-29									
	Prior Application Number: 60/083496									
	Prior Filing Date: 1998-04-29									
	Prior Application Number: 60/083499									
	Prior Filing Date: 1998-04-29									
	Prior Application Number: 60/083545									
	Prior Filing Date: 1998-04-29									
	Prior Application Number: 60/083554									
	Prior Filing Date: 1998-04-29									
	Prior Application Number: 60/083558									
	Prior Filing Date: 1998-04-29									
	Prior Application Number: 60/083559									
	Prior Filing Date: 1998-04-29									
	Prior Application Number: 60/083500									
	Prior Filing Date: 1998-04-29									
	Prior Application Number: 60/083742									
	Prior Filing Date: 1998-04-30									
	Prior Application Number: 60/084366									
	Prior Filing Date: 1998-05-05									
	Prior Application Number: 60/084414									
	Prior Filing Date: 1998-05-06									
	Prior Application Number: 60/084441									
	Prior Filing Date: 1998-05-06									
	Prior Application Number: 60/084637									
	Prior Filing Date: 1998-05-07									
	Prior Application Number: 60/084639									
	Prior Filing Date: 1998-05-07									
	Prior Application Number: 60/084640									
	Prior Filing Date: 1998-05-07									
	Prior Application Number: 60/084598									
	Prior Filing Date: 1998-05-07									
	Prior Application Number: 60/084600									
	Prior Filing Date: 1998-05-07									
	Prior Application Number: 60/084627									
	Prior Filing Date: 1998-05-07									
	Prior Application Number: 60/084643									
	Prior Filing Date: 1998-05-07									
	Prior Application Number: 60/085339									
	Prior Filing Date: 1998-05-13									
	Prior Application Number: 60/085338									
	Prior Filing Date: 1998-05-13									

oy



Db 1468 GTTTCATCTGCGCCCTACCTTCTAGGTGTCAACACCTGGAATCAATTGGCTCTTGCCT 1527  
Qy 1244 TATATCATGAAGTTCCTCCGCTAAACCGGCGCGATGAGAAAGAAACCATCACTAAGATG 1303  
Db 1528 TAT----- 1330  
Qy 1304 CTCTGGAGTACCGGACCCCTTTGAATATACCAAGAGGAGTACCACTTGTGGTGAG 1363  
Db 1531 -----AATATCACCAGGAGGAGTACCACTTGTGGTGAG 1566  
Qy 1364 GAGTACCTGGACAATGTCAATGAGCATGACTGGAGATGCTACGAACCCGTATGATGGAC 1423  
Db 1567 GAGTACCTGGACAATGTCAATGAGCATGACTGGAGATGCTACGAACCCGTATGATGGAC 1626  
Qy 1424 ATAGTTCAAGATGCCACTTTCTGTATGCCACACTGCAGACTGCTCACTACCCAGAT 1483  
Db 1627 ATAGTTCAAGATGCCACTTTCTGTATGCCACACTGCAGACTGCTCACTACCCAGAT 1683  
Qy 1484 GCCGCTCCCTCTACCTGTATGAATTTGAGCACCACTCGTGGAAATATCGTCAA 1543  
Db 1684 ----- 1683  
Qy 1544 CCCGCACTGATGGGCGAGACCATGGGATGAGATGACTTCTCTTTGGGGGCCCCCTTC 1603  
Db 1684 ----- 1683  
Qy 1604 GCCACAGCCTTTCATGGGTAGGAGAGCAGCCTTAGCTCCAGATGATGAATACTGG 1663  
Db 1684 ----- 1683  
Qy 1664 GCCAACTTGGCCGACAGAGAAACCCCAATGATGGGAATCTGCCCTGGCCACGCTAC 1723  
Db 1684 -----GAAACCCCAATGATGGGAATCTGCCCTGGCCACGCTAC 1724  
Qy 1724 AACAGGATGAAGTACCTGCAGCTGGATTTACCAAGAGTGGGATGAAGCTCAAG 1783  
Db 1725 AACAGGATGAAGTACCTGCAGCTGGATTTACCAAGAGTGGGATGAAGCTCAAG 1784  
Qy 1784 GAGAGAGATGGCTTTTGTGATGAGTCTGACAGTCTCAAGACCTGAGAGCAGAGG 1843  
Db 1785 GAGAGAGATGGCTTTTGTGATGAGTCTGACAGTCTCAAGACCTGAGAGCAGAGG 1844  
Qy 1844 CAATTTAAGGTTGGCTATGACAGAGGAGCCAAAGAGGGTTTGGCCCCACCATCCAGG 1903  
Db 1845 CAATTTAAGGTTGGCTATGACAGAGGAGCCAAAGAGGGTTTGGCCCCACCATCCAGG 1904  
Qy 1904 CCCTGGGAGACTAGCCATGACATACCTGGGACAGAGTTCTACCCA 1952  
Db 1905 CCCTGGGAGACTAGCCATGACATACCTGGGACAGAGTTCTACCCA 1953

## RESULT 6

US-09-978-697-253  
; Sequence 253, Application US/09978697  
; Patent No. US20020169284A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Fliviaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavin, Ivar J.

APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2830PIC27  
CURRENT APPLICATION NUMBER: US/09/978,697  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
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PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01



1	PRIOR APPLICATION NUMBER: 60/080328
2	PRIOR FILING DATE: 1998-04-01
3	PRIOR APPLICATION NUMBER: 60/080333
4	PRIOR FILING DATE: 1998-04-01
5	PRIOR APPLICATION NUMBER: 60/080334
6	PRIOR FILING DATE: 1998-04-01
7	PRIOR APPLICATION NUMBER: 60/081070
8	PRIOR FILING DATE: 1998-04-08
9	PRIOR APPLICATION NUMBER: 60/081049
10	PRIOR FILING DATE: 1998-04-08
11	PRIOR APPLICATION NUMBER: 60/081071
12	PRIOR FILING DATE: 1998-04-08
13	PRIOR APPLICATION NUMBER: 60/081195
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19	PRIOR APPLICATION NUMBER: 60/081955
20	PRIOR FILING DATE: 1998-04-15
21	PRIOR APPLICATION NUMBER: 60/081817
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23	PRIOR APPLICATION NUMBER: 60/081819
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25	PRIOR APPLICATION NUMBER: 60/081952
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28	PRIOR FILING DATE: 1998-04-15
29	PRIOR APPLICATION NUMBER: 60/082568
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33	PRIOR APPLICATION NUMBER: 60/082704
34	PRIOR FILING DATE: 1998-04-22
35	PRIOR APPLICATION NUMBER: 60/082804
36	PRIOR FILING DATE: 1998-04-22
37	PRIOR APPLICATION NUMBER: 60/082700
38	PRIOR FILING DATE: 1998-04-22
39	PRIOR APPLICATION NUMBER: 60/082797
40	PRIOR FILING DATE: 1998-04-22
41	PRIOR APPLICATION NUMBER: 60/082796
42	PRIOR FILING DATE: 1998-04-23
43	PRIOR APPLICATION NUMBER: 60/083336
44	PRIOR FILING DATE: 1998-04-27
45	PRIOR APPLICATION NUMBER: 60/083322
46	PRIOR FILING DATE: 1998-04-28
47	PRIOR APPLICATION NUMBER: 60/083392
48	PRIOR FILING DATE: 1998-04-29
49	PRIOR APPLICATION NUMBER: 60/083495
50	PRIOR FILING DATE: 1998-04-29
51	PRIOR APPLICATION NUMBER: 60/083496
52	PRIOR FILING DATE: 1998-04-29
53	PRIOR APPLICATION NUMBER: 60/083499
54	PRIOR FILING DATE: 1998-04-29
55	PRIOR APPLICATION NUMBER: 60/083545
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57	PRIOR APPLICATION NUMBER: 60/083554
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60	PRIOR FILING DATE: 1998-04-29
61	PRIOR APPLICATION NUMBER: 60/083559
62	PRIOR FILING DATE: 1998-04-29
63	PRIOR APPLICATION NUMBER: 60/083500
64	PRIOR FILING DATE: 1998-04-29
65	PRIOR APPLICATION NUMBER: 60/083742
66	PRIOR FILING DATE: 1998-04-30
67	PRIOR APPLICATION NUMBER: 60/084366
68	PRIOR FILING DATE: 1998-05-05
69	PRIOR APPLICATION NUMBER: 60/084414
70	PRIOR FILING DATE: 1998-05-06
71	PRIOR APPLICATION NUMBER: 60/084441
72	PRIOR FILING DATE: 1998-05-06
73	PRIOR APPLICATION NUMBER: 60/084637

;; PRIOR APPLICATION NUMBER: 60/0882804  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/0882700

PRIOR APPLICATION NUMBER: 60/082700	PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082797	PRIOR FILING DATE: 1998-04-22	PRIOR APPLICATION NUMBER: 60/082796	PRIOR FILING DATE: 1998-04-23	PRIOR APPLICATION NUMBER: 60/083336	PRIOR FILING DATE: 1998-04-27	PRIOR APPLICATION NUMBER: 60/083322	PRIOR FILING DATE: 1998-04-28	PRIOR APPLICATION NUMBER: 60/083392	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083495	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083496	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083499	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083545	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083554	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083558	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083559	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083500	PRIOR FILING DATE: 1998-04-29	PRIOR APPLICATION NUMBER: 60/083742	PRIOR FILING DATE: 1998-04-30	PRIOR APPLICATION NUMBER: 60/084366	PRIOR FILING DATE: 1998-05-05	PRIOR APPLICATION NUMBER: 60/084414	PRIOR FILING DATE: 1998-05-06	PRIOR APPLICATION NUMBER: 60/084441	PRIOR FILING DATE: 1998-05-06	PRIOR APPLICATION NUMBER: 60/084637
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Db 868 CCGGAGGCGCCTTCACTCGTGGCGCTCTCTTCTGACGAGGCTCTGACTTGGCCGCC 927  
Qy 644 CCGGAGAAAGTGGTCTGGTCTTCTGACGACAGGCTCGGCATCTTCGGCTTCTGAGC 703  
Db 928 CCGGAGAAAGTGGTCTGGTCTTCTGACGACAGGCTCGGCATCTTCGGCTTCTGAGC 987  
Qy 704 ACGGACGACAGCAGCAGCGCGGGGAACTGGGGGCTGCTGGACAGATGGGGCTCTCGGC 763  
Db 988 ACGGACGACAGCAGCAGCGCGGGGAACTGGGGGCTGCTGGACAGATGGGGCTCTCGGC 1047  
Qy 764 TGGGTGACGAGAAACATCGACGCTTCGGGGGAGACCCAGGAAATGTGACCTTTCGGC 823  
Db 1048 TGGGTGACGAGAAACATCGACGCTTCGGGGGAGACCCAGGAAATGTGACCTTTCGGC 1107  
Qy 824 CAGTCGGCGGGGCCATGAGCATCTCAGGACTGATGATCACCCTAGCTCGGGTCTC 893  
Db 1108 CAGTCGGCGGGGCCATGAGCATCTCAGGACTGATGATCACCCTAGCTCGGGTCTC 1167  
Qy 884 TTCATCGGGCCATTTCCAGAGTGGCACCCGCTTATTCAGACTTTTCATCACTAGTAAC 943  
Db 1168 TTCATCGGGCCATTTCCAGAGTGGCACCCGCTTATTCAGACTTTTCATCACTAGTAAC 1227  
Qy 944 CCATGAAGTGGCCAGAGGTTGCCACCTGCTGGATGCAACCAACAGCACAG 1003  
Db 1228 CCATGAAGTGGCCAGAGGTTGCCACCTGCTGGATGCAACCAACAGCACAG 1287  
Qy 1004 ATCTGTGTAATCTGCTGAGGCACTATCAGGACCAAGGTGATGCTGTGTCCAAAG 1063  
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Qy 1064 ATGAGATCTCCAACTGAACTTCAGAGAGACCCGGAAGATATCTGGTCCATGAGC 1123  
Db 1348 ATGAGATCTCCAACTGAACTTCAGAGAGACCCGGAAGATATCTGGTCCATGAGC 1407  
Qy 1124 CTTGTGTGGATGCTGTGTGATCCAGATGACCTTTGTGTCTCTGACCCAGGGGAG 1183  
Db 1408 CTTGTGTGGATGCTGTGTGATCCAGATGACCTTTGTGTCTCTGACCCAGGGGAG 1467  
Qy 1184 GTTTCATCTGTCCTACCTTCTAGGTGTCAACAACTGGAATTCATTTGGCTCTTGCCT 1243  
Db 1468 GTTTCATCTGTCCTACCTTCTAGGTGTCAACAACTGGAATTCATTTGGCTCTTGCCT 1527  
Qy 1244 TATATCATGAAGTTCCTCGCTAAACCGGCGAGTGAAGAAACCATCATAGATG 1303  
Db 1528 TAT----- 1530  
Qy 1304 CTCTGGAGTACCGCACCTCTTGAATATCACCAGGAGGAGTACCCTTTGTGGTGGAG 1363  
Db 1531 -----ATATCACCAGGAGGAGTACCCTTTGTGGTGGAG 1566  
Qy 1364 GAGTACCTGACATGTCATGACATGACATGACATGACATGACATGACATGACATGACAT 1423  
Db 1567 GAGTACCTGACATGTCATGACATGACATGACATGACATGACATGACATGACATGACAT 1626  
Qy 1424 ATAGTTCAAGATGCGACTTTCGTGTATGCCACACTGCACTGCTCACTACCAACAGAT 1483  
Db 1627 ATAGTTCAAGATGCGACTTTCGTGTATGCCACACTGCACTGCTCACTACCAACAGAT 1683  
Qy 1484 GCGGCTCCTCTCTACCTGTATGAATTTGAGCAGCAGCTCGTGGGAATATCGTCAA 1543  
Db 1684 ----- 1683  
Qy 1544 CCGGCACTGATGGGCGAGACCATGGGATGATGATGATGATGATGATGATGATGATGAT 1603  
Db 1684 ----- 1683  
Qy 1604 GCCACAGCCTTTCATGGGTAAAGAGAGGCACTTAGCTCCAGATGATGAATACTGG 1663  
Db 1684 ----- 1683  
Qy 1664 GCCAACTTGGCGGACAGGAAACCCCAATGATGGAATCTGCCCTGCTGGCCACGCTAC 1723  
Db 1684 -----GAAACCCCAATGATGGAATCTGCCCTGCTGGCCACGCTAC 1724

Qy 1724 AACAGAGTAAAAAGTACCTGCAGCTGGATTTTACCAAGAGTGGGATGAAGTCAAG 1783  
Db 1725 AACAGAGTAAAAAGTACCTGCAGCTGGATTTTACCAAGAGTGGGATGAAGTCAAG 1784  
Qy 1784 GAGAGAGATGCTTTTGGATGATGCTGTACCAAGTCTCAAGACCTTGAGAGCAGAGG 1843  
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Qy 1844 CAATTCTAAGGCTGCTATGACGAGGAGGACCAAGAGGGGTTTCCCCCACCACATCCAGG 1903  
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Qy 1904 CCCTGGGAGACTGACCATGGACATACCTGGGAGCAAGAGTCTTACCCA 1952  
Db 1905 CCCTGGGAGACTAGCCATGGACATACCTGGGAGCAAGAGTCTTACCCA 1953

## RESULT 7

US-09-978-192A-253  
; Sequence 253, Application US/09978192A  
; Patent No. US20020177553A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gottard, Audrey E.  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C9  
; CURRENT APPLICATION NUMBER: US/09/978,192A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/066364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077641  
; PRIOR FILING DATE: 1998-03-11  
; PRIOR APPLICATION NUMBER: 60/077649  
; PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER:	60/077791
PRIOR FILING DATE:	1998-03-12
PRIOR APPLICATION NUMBER:	60/078004
PRIOR FILING DATE:	1998-03-13
PRIOR APPLICATION NUMBER:	60/078886
PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/078936
PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/078910
PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/078939
PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/079294
PRIOR FILING DATE:	1998-03-25
PRIOR APPLICATION NUMBER:	60/079656
PRIOR FILING DATE:	1998-03-26
PRIOR APPLICATION NUMBER:	60/079664
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PRIOR APPLICATION NUMBER:	60/079663
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PRIOR APPLICATION NUMBER:	60/079728
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PRIOR APPLICATION NUMBER:	60/079786
PRIOR FILING DATE:	1998-03-27
PRIOR APPLICATION NUMBER:	60/079920
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PRIOR APPLICATION NUMBER:	60/079923
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PRIOR APPLICATION NUMBER:	60/080194
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PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/082568
PRIOR FILING DATE:	1998-04-21
PRIOR APPLICATION NUMBER:	60/082569
PRIOR FILING DATE:	1998-04-21
PRIOR APPLICATION NUMBER:	60/082704

Query Match 51.1%; Score 1013; DB 9; Length 2456;

Best Local Similarity 78.2%; Pred. No. 2.7e-292; Mismatches 0; Indels 403; Gaps 3;

Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;

QY	224	GGTCTTGGACACCAAGAGGCTCAAGTGTGACCAAAATATGGAACCTCGAAGGAAA	283
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QY	284	CAGATGCAATGGGGAAGACACCAATCAAGTCTTTTAGAGTCCCTTTCAGACCT	343
DB	448	CAGATGCAATGGGGAAGACACCAATCAAGTCTTTTAGAGTCCCTTTCAGACCT	507
QY	344	CCTCTAGGTATCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAAGGAATCAGA	403
DB	508	CCTCTAGGTATCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAAGGAATCAGA	567
QY	404	GATGCTACCACTACCCGCTG-----	425
DB	568	GATGCTACCACTACCCGCTGAGTGGAGTCTCGTCTGTCGCCAGGCTGGAGTGCAGTG	627
QY	426	-----	425
DB	628	GCAGATCTCGGCTCACTGCAACCTCCGCTCCCGGGTTCAAGCGAGTCTCCTGCCTCAG	687
QY	426	-----	425
DB	688	CCTCTAGTGTCTGGGCTACAGGTGCTGTCAGGAGTCTTGGGCGCAGCTGGGCTCGATG	747
QY	464	TACGTACAGACCGCGGAACGTTACAGTGGCTGGCTTTCAGCGAGGACTCTCTGTACCTG	523
DB	748	TACGTACAGACCGCGGAACGTTACAGTGGCTGGCTTTCAGCGAGGACTCTCTGTACCTG	807
QY	524	AACGTGTACG	583
DB	808	AACGTGTACG	867
QY	584	CCGGAGCGCGCTTATCTGCTGGCGCTGCTTCTCTGTCAGAGGCTCTGACCTTGGCGGC	643
DB	868	CCGGAGCGCGCTTATCTGCTGGCGCTGCTTCTCTGTCAGAGGCTCTGACCTTGGCGGC	927
QY	644	CGCAGAAAGT	703
DB	928	CGCAGAAAGT	987
QY	704	ACGACACACACACG	763
DB	988	ACGACACACACACG	1047
QY	764	TGGGTGACAGGAAATCGACGCTTCCGCGGAGACCCAGGAAATGTGACCTGTTCGCG	823
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DB	1108	CAGTCCG	1167
QY	884	TTCCATCGGCGCATTTCCAGAGTGGCAGCGGTTATTCAGCTTTTTCATCACTAGTAC	943
DB	1168	TTCCATCGGCGCATTTCCAGAGTGGCAGCGGTTATTCAGCTTTTTCATCACTAGTAC	1227
QY	944	CCACTGAAAGTGGCAAGAGTGGTCCCACTGCTGATGCAACCAACAGCAGCAGAC	1003
DB	1228	CCACTGAAAGTGGCAAGAGTGGTCCCACTGCTGATGCAACCAACAGCAGCAGAC	1287
QY	1004	ATCTGTAACTGCTGAGGCACTATCAGGACCAAGGTGATGGTGTTCACACAG	1063
DB	1288	ATCTGTAACTGCTGAGGCACTATCAGGACCAAGGTGATGGTGTTCACACAG	1347
QY	1064	ATGAGATTCCTCAACTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGC	1123
DB	1348	ATGAGATTCCTCAACTGAACTTCCAGAGAGACCCGGAAGAGATTATCTGGTCCATGAGC	1407

RESULT 8

US-09-999-932A-253

; Sequence 253, Application US/09999932A

; Publication No. US20020192706A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnovers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Geiber, Hanspeter

APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
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APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
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APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PLC63  
CURRENT APPLICATION NUMBER: US/09/999,832A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
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PRIOR FILING DATE: 1998-03-11  
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Query Match 51.1%; Score 1013; DB 9; Length 2456;  
Best Local Similarity 78.2%; Pred. NO. 2.7e-292;  
Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;

224	QY	GGTGCTTGCACACCAAGAGGCCTCAAGTGTCTACCAAAATATGGAACCCCTGCAAGAAAA	283
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284	QY	CAGATGCATGTGGGAAGACACCCATCCAAGTCTTTTATAGAGTCCCTTCTCCAGACCT	343
448	Db	CAGATGCATGTGGGAAGACACCCATCCAAGTCTTTTATAGAGTCCCTTCTCCAGACCT	507
344	QY	CCTCTAGGTATCCTCAGGTTTGCACCTTCAGAACCCCGAGGCCCTGGAAAGGAATCAGA	403
508	Db	CCTCTAGGTATCCTCAGGTTTGCACCTTCAGAACCCCGAGGCCCTGGAAAGGAATCAGA	567
404	QY	GATGCTACCACTATCCGCCCTG-----	425
568	Db	GATGCTACCACTATCCGCCCTGGATGGAGTCTGCTCTGCGCAGCGCTGGAGTGCAGTG	627
426	QY	-----	425
628	Db	GCACGATCTCGGCTCACTGCAACCTCGCGCTCCCGGTTTCAAGCGAGTCTCCTGCCTCAG	687
426	QY	-----GGTGGCTGCAGGAGTCTCGGGGCAGCTGGCCCTCGATG	463
688	Db	CCTCTGAGTGTCTGGGGCTACAGTGTCTGAGGAGTCTTGGGGGCAGCTGGCCCTCGATG	747
464	QY	TACGTCAAGACGCGGGAAACGCTACAAGTGGCTCGGCTTCAGCGAGACTGTCTGTACCTTG	523
748	Db	TACGTCAAGACGCGGGAAACGCTACAAGTGGCTCGGCTTCAGCGAGACTGTCTGTACCTTG	807

Qy 1604 GCCACAGGCTTTCCATGGGTAAGGAGGCACTTAGCCTCCAGATGATGAATACTGG 1663  
Db 1684 ----- 1683  
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Db 1684 -----GAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTAC 1724  
Qy 1724 AACAGGATGAAAGTAGCTGACCTGAGTGTGATTTTACCACAAGAGTGGGCATGAAGCTCAAG 1783  
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RESULT 9

US-09-978-189-253  
; Sequence 253, Application US/09978189  
; Publication No. US20030004102A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P17  
; CURRENT APPLICATION NUMBER: US/09/978,189  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
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RESULT 10

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; Sequence 253, Application US/09978608A  
; Publication No. US20030045462A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David

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; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Oiang
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
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; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
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; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PLC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
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; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-978-608A-253

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RESULT 11

US-09-978-585A-253  
 ; Sequence 253, Application US/09978585A  
 ; Publication No. US20030049633A1  
 ; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
 APPLICANT: Baker Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan  
 APPLICANT: Ferrara, Napoleon  
 APPLICANT: Filvaroff, Ellen  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gao, Wei-Qiang  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Hillan, Kenneth J.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Kuo, Sophia S.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Shelton, David L.  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 TITLE OF INVENTION: Acids Encoding the Same  
 FILE REFERENCE: P2630P15  
 CURRENT APPLICATION NUMBER: US/09/978,585A  
 CURRENT FILING DATE: 2001-10-16  
 NUMBER OF SEQ ID NOS: 624  
 Prior Application removed - See File Wrapper or Palm  
 SEQ ID NO 253  
 LENGTH: 2456  
 TYPE: DNA  
 ORGANISM: Homo sapiens

US-09-978-585A-253

Query Match 51.1%; Score 1013; DB 10; Length 2456;  
 Best Local Similarity 78.2%; Pred. No. 2.7e-292;  
 Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;  
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 524 AAGTGTACGCGCGGCGCGCGCGCGGATCCCGAGCTGCGAGTGTCTGCTGCTTC 583  
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 1567 GAGTACCTGGACAATGCAATGAGCATGATGGAAGATGCTACGAAACCTGTATGATGGAC 1626  
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 1904 CCCTGGGAGAGTACCTAGCCTAGCCTAGCCTAGCCTAGCCTAGCCTAGCCTAGCCTAGCCT 1952  
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RESULT 12  
 US-09-978-191A-253  
 ; Sequence 253, Application US/09978191A  
 ; Publication No. US20030050239A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary B.  
 ; APPLICANT: Goddard, Audrey  
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 ; APPLICANT: Grimaldi, J. Christopher  
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 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kijavie, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James;

APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C4  
CURRENT APPLICATION NUMBER: US/09/978,191A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
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PRIOR APPLICATION NUMBER: 60/084637  
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; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697
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Query Match      51.1%; Score 1013; DB 10; Length 2456;
Best Local Similarity 78.2%; Pred. No. 2.7e-292;
Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;

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Qy 404 GATGCTACCACTACCCGCTG----- 425
Db 568 GATGCTACCACTACCCGCTGGATGGAGTCTCGCTCTGTGCGCAGGCTGGAGTGCAGTG 627

Qy 426 ----- 425
Db 628 GCACGATCTCGGCTCACTGCAACCTCGCCCTCGGGGTTCAGCGAGTCTCTGCTCAG 687

Qy 426 -----GGTGGCTGACAGAGTCTCTGGGCGCCAGCTGGCTCGATG 463
Db 688 CCTCTGAGTGTCTGGGCTACAGTGTCTGACAGAGTCTCTGGGCGCCAGCTGGCTCGATG 747

Qy 464 TACGTACGACGCGGGAACGATCAAGTGGTGGCTTTCAGCGAGGAGTCTGTGTACCTG 523
Db 748 TACGTACGACGCGGGAACGATCAAGTGGTGGCTTTCAGCGAGGAGTCTGTGTACCTG 807

Qy 524 AACGTGTACGCGCGCGCGCGGATCCCGAGTCCCGAGTGGCTGATGGTCTGGTTC 583
Db 808 AACGTGTACGCGCGCGCGCGGATCCCGAGTCCCGAGTGGCTGATGGTCTGGTTC 867

Qy 584 CCGGAGGCGCTTTCATGCTGGGCGCTTCTTTCGTACGAGGCTCTGACTTGGCGGCC 643
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Qy 644 CGCGAAGAGTGGTGGTCTTCTTCGACGACAGGCTCGGCATCTTCGGCTTCTCGAGC 703

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Qy 1084 ATGAGATTCCTCCAACTGCTTCGAGAGACCCGGAAGAGATTTCTGGTCCATGAGC 1123
Db 1348 ATGAGATTCCTCCAACTGCTTCGAGAGACCCGGAAGAGATTTCTGGTCCATGAGC 1407
Qy 1124 CTTGTGGTGGATGGTGTGCTGATCCAGATGACCTTTTGGTGTCTGACCCAGGGGAAG 1183
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Qy 1244 TATATCATGAAGTTCCTCGCTAAACCGGCGAGCGGATGAGAAAGGAAACCATCACTAAGATG 1303
Db 1528 TAT----- 1530
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Db 1567 GAGTACCTGGACAAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGGTATGATGAC 1626
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Db 1627 ATAGTTCAAGATGCCACTTTCTGTATGCCACACTGCAGACTGTCTACTACCCAGAT 1683
Qy 1484 GCGGCGCTCTCTGTCTACTGTATGAATTTGAGGACACCGCTCGTGGGAATTAATCGTCAA 1543
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Db 1684 ----- 1683
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; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: E2630P1C17  
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; CURRENT FILING DATE: 2002-03-19  
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Query Match

51.1%; Score 1013; DB 10; Length 2456;

Best Local Similarity 78.2%; Pred. No. 2.7e-292;  
Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;  
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DB 388 GGTGCTTTGCACACCAAGAGGCTCAAGTGGTACCAAAATATGGAACCTGCAAGGAAA 447  
QY 284 CAGATGATGTGGGGAAGACACCCATCAAGTCTTTTGGAGTCCCTTCTCCAGACCT 343  
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QY 344 CCTCTAGGTATCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGA 403  
DB 508 CCTCTAGGTATCTCAGGTTTGCACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGA 567  
QY 404 GATGCTACCACTACCGCCCTG----- 425  
DB 568 GATGCTACCACTACCGCCCTGGAAGGAGTCTCGCTCTGTGCCAGCGTGGAGTGCAGTG 627  
QY 426 ----- 425  
DB 628 GCACGATCTCGGCTCACTGCAACCTCCGCTCCCGGGTTCAAGCGAGTCTCTCTGCCTCAG 687  
QY 426 -----GGTGCCTGAGAGTCTCTGGGCCAGCTGGGCCCTCGATG 463  
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QY 464 TACGTCACGACGCGGGAACGTTACAAGTGGCTCGGCTTACGAGGAGTCTGTGTACCTG 523  
DB 748 TACGTCACGACGCGGGAACGTTACAAGTGGCTCGGCTTACGAGGAGTCTGTGTACCTG 807  
QY 524 AACGTGTACG 583  
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QY 764 TGGGTGCAGGAGAACATCGAGCCTTTCGGGGGAGACCCAGGAAATGTGACCCCTGTTCGCG 823  
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QY 824 CAGTCGGCGGGGCGCATGAGCATCTCAGACTGATGATGTACCCCTAGCCTCGGCTCTC 883  
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QY 884 TTCCATCGGGCCATTTCCAGAGTGCACCGGTTTATTACAGACTTTTTCATCACTAGTAAC 943  
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Query Match 51.1%; Score 1013; DB 10; Length 2456;
Best Local Similarity 78.2%; Pred. No. 2.7e-292;
Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;
QY 224 GGTGCTTGCACACCAAGAGGCTCAAGTGTACCAATATGGAACCTCGAAGAAAA 283
Db 388 GGTGCTTGCACACCAAGAGGCTCAAGTGTACCAATATGGAACCTCGAAGAAAA 447
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Db 448 CAGATGCATGTGGGAAGACACCCATCCAGTCTTTTAGGAGTCCCTTCTCCAGACT 507
QY 344 CCTTAGGTATCCTCAGGTTTGACCTCCAGAACCCCGAGCCCTGGAAGAAATCAGA 403
Db 508 CCTTAGGTATCCTCAGGTTTGACCTCCAGAACCCCGAGCCCTGGAAGAAATCAGA 567
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QY 426 ----- 425
Db 628 GCACGATCTCGGCTCACTGCAACCTCCGCTCCCGGGTTCAGAGGAGTCTCTGCTCAG 687
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Db 688 CCTCTGAGTGTCTGGGGCTTACAGGTGCTTGGGGCCAGCTGGCCTCGATG 747
QY 464 TAGCTCAGCACCGGGAACGGTACAAAGTGGCTGCCCTTTCAGCGAGGACTGTGTACCTG 523
Db 748 TAGCTCAGCACCGGGAACGGTACAAAGTGGCTGCCCTTTCAGCGAGGACTGTGTACCTG 807
QY 524 AACGTGTACG 583



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29	29	PRIOR APPLICATION NUMBER: 60/079786	29	29	PRIOR FILING DATE: 1998-04-29
30	30	PRIOR FILING DATE: 1998-03-27	30	30	PRIOR APPLICATION NUMBER: 60/083558
31	31	PRIOR APPLICATION NUMBER: 60/079920	31	31	PRIOR FILING DATE: 1998-04-29
32	32	PRIOR FILING DATE: 1998-03-30	32	32	PRIOR APPLICATION NUMBER: 60/083559
33	33	PRIOR APPLICATION NUMBER: 60/079923	33	33	PRIOR FILING DATE: 1998-04-29
34	34	PRIOR FILING DATE: 1998-03-30	34	34	PRIOR APPLICATION NUMBER: 60/083500
35	35	PRIOR APPLICATION NUMBER: 60/080105	35	35	PRIOR FILING DATE: 1998-04-29
36	36	PRIOR FILING DATE: 1998-03-31	36	36	PRIOR APPLICATION NUMBER: 60/083742
37	37	PRIOR APPLICATION NUMBER: 60/080107	37	37	PRIOR FILING DATE: 1998-04-30
38	38	PRIOR FILING DATE: 1998-03-31	38	38	PRIOR APPLICATION NUMBER: 60/084366
39	39	PRIOR APPLICATION NUMBER: 60/080165	39	39	PRIOR FILING DATE: 1998-05-05
40	40	PRIOR FILING DATE: 1998-03-31	40	40	PRIOR APPLICATION NUMBER: 60/084414
41	41	PRIOR APPLICATION NUMBER: 60/080194	41	41	PRIOR FILING DATE: 1998-05-06
42	42	PRIOR FILING DATE: 1998-03-31	42	42	PRIOR APPLICATION NUMBER: 60/084441
43	43	PRIOR APPLICATION NUMBER: 60/080327	43	43	PRIOR FILING DATE: 1998-05-06
44	44	PRIOR FILING DATE: 1998-04-01	44	44	PRIOR APPLICATION NUMBER: 60/084637
45	45	PRIOR APPLICATION NUMBER: 60/080328	45	45	PRIOR FILING DATE: 1998-05-07
46	46	PRIOR FILING DATE: 1998-04-01	46	46	PRIOR APPLICATION NUMBER: 60/084639
47	47	PRIOR APPLICATION NUMBER: 60/080333	47	47	PRIOR FILING DATE: 1998-05-07
48	48	PRIOR FILING DATE: 1998-04-01	48	48	PRIOR APPLICATION NUMBER: 60/084640
49	49	PRIOR APPLICATION NUMBER: 60/080334	49	49	PRIOR FILING DATE: 1998-05-07
50	50	PRIOR FILING DATE: 1998-04-01	50	50	PRIOR APPLICATION NUMBER: 60/084598
51	51	PRIOR APPLICATION NUMBER: 60/081070	51	51	PRIOR FILING DATE: 1998-05-07
52	52	PRIOR FILING DATE: 1998-04-08	52	52	PRIOR APPLICATION NUMBER: 60/084600
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56	56	PRIOR FILING DATE: 1998-04-08	56	56	PRIOR APPLICATION NUMBER:

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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      51.1%; Score 1013; DB 10; Length 2456;
Best Local Similarity 78.2%; Pred. No. 2.7e-292;
Matches 1446; Conservative 0; Mismatches 0; Indels 403; Gaps 3;

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DB 448 CAGATGCATGTGGGGAAGACACCCATCCAAAGTCTTTTAGAGTCCCTTCTCCAGACCT 507
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DB 508 CCTTAGGTATCCCTCAGTTTGCACCTCCAGAACCCCGGAGGCCCTGGAAGGAATCAGA 567
QY 404 GATGCTACCACTACCCGCGCTG----- 425
DB 568 GATGCTACCACTACCCGCGCTGAGTGGAGTCTGCTCTGTGCGCAGGCTGGAGTGAGTG 627
QY 426 ----- 425
DB 628 GCACGATCTCGGCTCACTGCAACCTCCCGCCTCCCGGCTTCAAGCGAGTCTCCTGCCTCAG 687
QY 426 -----GTCGCTGCAGAGTCTCTGGGCGCAGCTGGGCTCGATG 463
DB 688 CCTCTGAGTGTCTGGGGGTACAGTGTCTGAGAGTCTCTGGGCGCAGCTGGGCTCGATG 747
QY 464 TACGTACAGCAGCGGGGAACGGTACAGTGTCTGCGCTTTCAGCAGAGACTGTCTGTACCTG 523
DB 748 TACGTACAGCAGCGGGGAACGGTACAGTGTCTGCGCTTTCAGCAGAGACTGTCTGTACCTG 807
QY 524 AACGTGTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 583
DB 808 AACGTGTACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 867
QY 584 CCGGAGCGCGCTTCACTGCTGGGCGCTCTTCTGTAAGAGGCTCTGACTTGGCGCGC 843
DB 868 CCGGAGCGCGCTTCACTGCTGGGCGCTCTTCTGTAAGAGGCTCTGACTTGGCGCGC 927
QY 644 CCGAGAGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 703
DB 928 CCGAGAGAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 987
QY 704 ACGGACGACAGCAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 763
DB 988 ACGGACGACAGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1047
QY 764 TGGGTGCAGGAGAACATTCGAGCCTTTCGGGGGAGACCCAGGAATGTGACCCCTGTTCGCG 823
DB 1048 TGGGTGCAGGAGAACATTCGAGCCTTTCGGGGGAGACCCAGGAATGTGACCCCTGTTCGCG 1107
QY 824 CAGTTCGGCGGGGCGCATGAGCATCTCAGGACTGATGATGATGATGATGATGATGATGATG 883
DB 1108 CAGTTCGGCGGGGCGCATGAGCATCTCAGGACTGATGATGATGATGATGATGATGATGATG 1167
QY 884 TTCCATCGGCGCAATTTCCAGAGTGGCAGCGCGTTTTCAGACTTTTCATCACTAGTAAC 943
DB 1168 TTCCATCGGCGCAATTTCCAGAGTGGCAGCGCGTTTTCAGACTTTTCATCACTAGTAAC 1227
QY 944 CCACTGAAGTGGCCCAAGAGTGGCCCACTGGCTGGATGACCAACAGCAGCAGCAG 1003
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QY 1004 ATCCTGTGTAACCTCCTGAGGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCCAACAG 1063
DB 1288 ATCCTGTGTAACCTCCTGAGGGGCACTATCAGGGACCAAGGTGATGCGTGTGTCCCAACAG 1347

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DB 1408 CTTGTGGTGGATGGTGTGATCCAGATGACCCCTTTGGTGTCTCTGACCCAGGGAAG 1467
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DB 1528 TAT----- 1530
QY 1304 CTCTGGAGTACCCGCACTCTGTTGAATATCAACAAAGGAGCAGGTACCACTTTGGTGGAG 1363
DB 1531 -----AATATCAACAAAGGAGCAGGTACCACTTTGGTGGAG 1566
QY 1364 GAGTACCTGGAACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTATGATGAGC 1423
DB 1567 GAGTACCTGGAACAATGTCAATGAGCATGACTGGAAGATGCTACGAAACCGTATGATGAGC 1626
QY 1424 ATAGTCAAGATGCGCACTTTCTGTATGCCACACTGCAGACTGTCTACTACCCAGAGAT 1483
DB 1627 ATAGTCAAGATGCGCACTTTCTGTATGCCACACTGCAGACTGTCTACTACCCAGAGAT 1683
QY 1484 GCCGCGCTCCCTGCTACTCTGTATGAATTTGAGCACCAGCTCGTGAATAATCGTCAA 1543
DB 1684 ----- 1683
QY 1544 CCCGCACTGATGGGGCAGACCATGGGGATGAGATGATCTCTCTTTGGGGGGCCCCCTTC 1603
DB 1684 ----- 1683
QY 1604 GCCACAGCCCTTTCATGGGTAAGGAGAGGCACTTAGCCTCCAGATGATGAATACTGCG 1663
DB 1684 ----- 1683
QY 1664 GCCAACTTTGGCCGCAACAGGAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTAC 1723
DB 1684 -----GAAACCCCAATGATGGGAATCTGCCCTGCTGGCCACGCTAC 1724
QY 1724 AACAGGATGAAAGTACCTGCACTGATTTTACCAAGAGTGGGCATGAAGCTCAAG 1783
DB 1725 AACAGGATGAAAGTACCTGCACTGATTTTACCAAGAGTGGGCATGAAGCTCAAG 1784
QY 1784 GAGAAAGATGGCTTTTGGTGTGATGTGTACCAAGTCTCAAGACCTGAGAGACGAGG 1843
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QY 1844 CAATTCATAGGCTCGCTATGCAAGAGAGGCCAAAGAGGGGTTTGGCCCCCAGCAGG 1903
DB 1845 CAATTCATAGGCTCGCTATGCAAGAGAGGCCAAAGAGGGGTTTGGCCCCCAGCAGG 1904
QY 1904 CCCTGGGAGACTAGCCATGACATACCTGGGACAGAGTCTTACCCA 1952
DB 1905 CCCTGGGAGACTAGCCATGACATACCTGGGACAGAGTCTTACCCA 1953

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Search completed: August 11, 2004, 22:36:09  
Job time : 945.854 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

CM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 10:40:18 ; Search time 5212.08 Seconds  
(without alignments)  
11381.439 Million cell updates/sec

Title: US-10-001-227-1

Perfect score: 1983

Sequence: 1 ccttagccaattcgccga.....gtttaaacctgcaggactag 1983

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: em\_estba.\*

2: em\_esthum.\*

3: em\_estin.\*

4: em\_estmu.\*

5: em\_estov.\*

6: em\_estpl.\*

7: em\_estro.\*

8: em\_htc.\*

9: gb\_est1.\*

10: gb\_est2.\*

11: gb\_htc.\*

12: gb\_est3.\*

13: gb\_est4.\*

14: gb\_est5.\*

15: em\_estfun.\*

16: em\_estom.\*

17: em\_gss\_hum.\*

18: em\_gss\_inv.\*

19: em\_gss\_pln.\*

20: em\_gss\_vrt.\*

21: em\_gss\_fun.\*

22: em\_gss\_mam.\*

23: em\_gss\_mus.\*

24: em\_gss\_pro.\*

25: em\_gss\_rod.\*

26: em\_gss\_phg.\*

27: em\_gss\_vrl.\*

28: gb\_gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1073.2	54.1	2356	11 AK037191	AK037191 Mus muscu
2	900.4	45.4	3431	11 BC041823	BC041823 Homo sapi
3	825.4	41.6	988	12 EQ053090	EQ053090 AGENCOURT
4	761.2	38.4	1047	12 BM547028	BM547028 AGENCOURT

5	591.4	29.8	593	13 BQ269800	BQ269800 iX30C07.X
6	482.4	24.3	526	12 BI460262	BI460262 603201884
7	433	21.8	468	10 AW512144	AW512144 xus4e11.X
8	401.4	20.2	1918	14 CF111083	CF111083 Shultzomi
9	395	19.9	1944	11 AK078879	AK078879 Mus muscu
10	371.6	18.7	634	10 BB630313	BB630313 BB630313
11	363.8	18.3	403	9 AA450272	AA450272 zx42h02.r
12	346.6	17.5	478	14 CF1116765	CF1116765 ad555.z1
13	343	17.3	442	13 BX488287	BX488287 DPEZP86E
14	331.6	16.7	438	9 AI949486	AI949486 wq10h04.X
15	320	16.1	884	13 BX36837	BX36837 BX336837
16	319.2	16.1	710	10 BF126303	BF126303 601650490
17	319.2	16.1	1680	29 AY414459	AY414459 Homo sapi
18	309.8	15.6	881	13 BX397287	BX397287 BX397287
19	308.8	15.6	1438	14 CF111142	CF111142 Shultzomi
20	308.8	15.6	1438	14 CF111143	CF111143 Shultzomi
21	301.2	15.2	388	14 R85476	R85476 y037a09.s1
22	298.8	15.1	1680	29 AY414461	AY414461 Mus muscu
23	290.6	14.7	307	12 EG993190	EG993190 RC4-H1109
24	288.2	14.5	1050	10 BF236748	BF236748 602028044
25	285.2	14.4	2661	11 AK033563	AK033563 Mus muscu
26	283.6	14.3	2687	11 AK077248	AK077248 Mus muscu
27	274.8	13.9	1942	11 BC015286	BC015286 Mus muscu
28	270	13.6	731	12 BI761231	BI761231 603043472
29	266	13.4	1958	11 AK078953	AK078953 Mus muscu
30	264.8	13.4	4927	11 AK040349	AK040349 Mus muscu
31	264	13.3	731	13 EX095055	EX095055 BX095055
32	263.8	13.3	296	9 AA339398	AA339398 EST4476
33	261.8	13.2	412	10 BG013590	BG013590 CM4-GN036
34	259.6	13.1	621	9 AA865634	AA865634 og93h11.s
35	252.8	12.7	930	13 BQ716182	BQ716182 AGENCOURT
36	250	12.6	2038	11 EC019926	EC019926 Mus muscu
37	249	12.6	533	14 N44535	N44535 YV32C12.r1
38	239	12.1	257	10 BE831841	BE831841 RC6-M1006
39	231.6	11.7	650	14 CB468793	CB468793 734647 MA
40	231	11.6	904	13 BQ900930	BQ900930 AGENCOURT
41	228.2	11.5	472	14 N25091	N25091 YX18b11.r1
42	223.2	11.3	928	13 BQ900803	BQ900803 AGENCOURT
43	221.6	11.2	663	14 CB464960	CB464960 726212 MA
44	221.2	11.2	900	13 BU164515	BU164515 AGENCOURT
45	218.8	11.0	585	14 CB450706	CB450706 705389 MA

#### ALIGNMENTS

RESULT 1

AK037191

LOCUS

DEFINITION

Mus musculus 6 days neonate skin cDNA, RIKEN full-length enriched

library, clone: A030007M20 product: hypothetical Carboxylesterases

type-B containing protein, full insert sequence.

AK037191

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

AK037191 2356 bp mRNA linear HTC 19-SEP-2003  
Mus musculus 6 days neonate skin cDNA, RIKEN full-length enriched  
library, clone: A030007M20 product: hypothetical Carboxylesterases  
type-B containing protein, full insert sequence.

AK037191 GI:26085654  
HTC; CAP trapper.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.; Mus.

1  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
11042159







QY	1086	TC	CAGAGAGACCCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGTGGATGGTGTGGTGA	1145
DB	698	TC	CAGAGAGACCCCGGAAGAGATTATCTGGTCCATGAGCCCTGTGTGGATGGTGTGGTGA	757
QY	1146	TC	CAGATGACCCCTTTGGTGTCTCCTGACCCAGGGGAAGTTCATCTGTGCCCTACCTTC	1205
DB	758	TC	CAGATGACCCCTTTGGTGTCTCCTGACCCAGGGGAAGTTCATCTGTGCCCTACCTTC	817
QY	1206	TAG	GTCTCAACCACTGGGAATTCAAATTTGGCTCTTGCTTTATATCATGAAGTTC	1265
DB	818	TAG	GTCTCAACCACTGGGAATTCAAATTTGGCTCTTGCTTTATATCATGAAGTTC	877
QY	1266	AC	CGGACGCGATGAGAAAGGAACCATCAGTAAGATGCTCTGGAGTACCCACCGCTGT	1325
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DB	938	TG	939	
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BQ053090				
LOCUS				
DEFINITION	BQ053090	988 bp	mRNA	linear EST 29-MAR-2002
	AGENCOURT_6821751 NIH_MGC_106	Homo sapiens	cdna clone	IMAGE:5934661
	5', mRNA sequence.			
ACCESSION	BQ053090			
VERSION	BQ053090.1	GI:19812430		
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 988)			
AUTHORS	NIH-MGC <a href="http://mgs.nci.nih.gov/">http://mgs.nci.nih.gov/</a> ;			
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgabbs-r@mail.nih.gov">cgabbs-r@mail.nih.gov</a> Tissue Procurement: Dr. Daniel McVicar, DBS/NCI CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLCM2121 row: C column: 14 High quality sequence stop: 675. Location/Qualifiers			
FEATURES	1..988			
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	/mol_type="mRNA"			
	/db_xref="taxon:9606"			
	/clone="IMAGE:5934661"			
	/tissue_type="natural killer cells, cell line"			
	/lab_host="PH108 (phage-resistant)"			
	/clone_lib="NIH_MGC_106"			
	/note="Organ: Blood; Vector: pOTB7; Site 1: XhoI; Site 2: ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGCAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life technologies). Note: this is a NIH_MGC Library."			
ORIGIN				
Query Match	41.6%;	Score 825.4;	DB 12;	Length 988;
Best Local Similarity	97.2%;	Pred. No. 6e-183;		
Matches 881;	Conservative	0;	Mismatches 16;	Indels 9;
Gaps	4;			
QY	279	GA	AACAGATGATGT-GGGGAAGACACCCATCCAAAGCTTTTATGAGATCCCTTC	337



ORIGIN  
XhoI site was destroyed after directional cloning.  
Amplified once. Contact information: Hiroshi Inoue, MD,  
Metabolism Div. (Alan Permutt Lab), Washington University  
School of Medicine, Box 8127, 660 South Euclid Ave., St.  
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:  
314-362-1916, Fax: 314-747-2692."

Query Match 29.8%; Score 591.4; DB 13; Length 593;  
Best Local Similarity 99.8%; Pred. No. 4.9e-128;  
Matches 592; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db |||||  
QY 1 TGCAGGAGTCTGGGGCCAGCTGGCTCGATGATGACGACGCGGGGAAACGTTACAGT 60  
Db |||||  
QY 492 GGCTGGCTTTCAGCGAGGACTGTCTGTACCTGAACGTGTACGCGCGCGCGCGCGCG 551  
Db |||||  
QY 61 GGCTGGCTTTCAGCGAGGACTGTCTGTACCTGAACGTGTACGCGCGCGCGCGCGCG 120  
Db |||||  
QY 552 GGGATCCCGAGCTGCCAGTATGCTGTGTTCGGGAGGCGCTTTCATGCTGGGGCTG 611  
Db |||||  
QY 121 GGGATCCCGAGCTGCCAGTATGCTGTGTTCGGGAGGCGCTTTCATGCTGGGGCTG 180  
Db |||||  
QY 612 CTTCCTGCTACGAGGGCTCTGACTTGGCGCGCGCGAGAAAGTGGTGGTGTCTGCG 671  
Db |||||  
QY 181 CTTCCTGCTACGAGGGCTCTGACTTGGCGCGCGCGAGAAAGTGGTGGTGTCTGCG 240  
Db |||||  
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Db |||||  
QY 241 AGCAGAGCTCGGCATCTTCGGCTTCTGTAGCAGGACGACGCCGCGCGGGAAT 300  
Db |||||  
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QY 301 GGGGGCTGTGGACAGATGGCGGCTCTGCGTGGGTGAGGAGAACATCGCAGCTTCG 360  
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Db |||||  
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Db |||||  
QY 421 GACTGATGATGTACCCCTAGCTCGGGTCTTTCATCGGGCCATTTCCAGAGTGGCA 480  
Db |||||  
QY 912 CCGGTTATTCAGACTTTTCATCACTAGTAACCCACTGAAGTGGCCAGAGGTTGCC 971  
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QY 481 CCGGTTATTCAGACTTTTCATCACTAGTAACCCACTGAAGTGGCCAGAGGTTGCC 540  
Db |||||  
QY 972 ACCTGGCTGATCAACCAACAGACACAGATCTCGTAACTGCCTGAGG 1024  
Db |||||  
QY 541 ACCTGGCTGATCAACCAACAGACACAGATCTCGTAACTGCCTGAAG 593  
Db |||||

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VERSION BI460262.1 GI:15250918  
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ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 526)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-r@mail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki

Toshiyuki and Piero Carninci (RIKEN)  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L2AM11675 row: 5 column: 22  
High quality sequence stop: 525.  
Location/Qualifiers  
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primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NIH/NHGRI, National Institutes of Health). Note: this is  
a NIH\_MGC Library."

FEATURES  
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1 (bases 1 to 468)  
NCI-CCGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgaps@mail.nih.gov](mailto:cgaps@mail.nih.gov)  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINL at:  
[image.llnl.gov/image/html/iresources.shtml](http://image.llnl.gov/image/html/iresources.shtml)  
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1 (bases 1 to 1918)  
Shultz, M.A., Zhang, J., Gu, Y.-Z., Baker, G.L., Fannuchi, M.V.,  
Padua, A.M., Gurske, W.A., Morin, D., Penn, S.G., Jovanovich, S.B.,  
Plopper, C.G. and Buckpitt, A.R.  
Gene Expression Analysis in Response to Lung Toxicants: I.  
Sequencing and Microarray Development  
Unpublished (2003)  
Contact: Shultz, MA  
Dept. of Molecular Biosciences, School of Veterinary Medicine  
University of California, Davis  
1311 Haring Hall, One Shields Avenue, Davis, CA 95616, USA  
Tel: 530 752 0793  
Fax: 530 752 4698  
Email: [mashultz@ucdavis.edu](mailto:mashultz@ucdavis.edu)  
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Qy 434 CAGGAGTCTCTTGGGGCCAGTGGCTCTGATGTAGTCAGCACGCGGGAACGGTACAAG 490  
Db 296 CAAGATGCTGTTGGAGGGCAGGTTCTCTCAGAGCTTTTCCACCAAGAGGAACATTT 355  
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DEFINITION

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VERSION  
KEYWORDS  
SOURCE  
ORGANISM

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AK078879 1944 bp mRNA linear HTC 18-SEP-2003  
Mus musculus adult male colon cDNA, RIKEN full-length enriched  
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AK078879.1 GI:26347580  
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Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci,P. and Hayashizaki,Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349636

2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Sasaki,N., Carninci,P.,  
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20493374  
11042159

3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M.,  
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,  
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,  
Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,  
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,Y.,  
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multichipillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

5 The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 1944)

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,  
Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,  
Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,T., Kasukawa,T.,  
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Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,  
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Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,  
Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,  
Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
Muramatsu,M. and Hayashizaki,Y.

## TITLE

## JOURNAL

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail:genome-res@gsr.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)

## COMMENT

cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.

Please visit our web site for further details.

URL:http://genome.gsc.riken.go.jp/

URL:http://fantom.gsc.riken.go.jp/.

## FEATURES

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## polyA\_site

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QY 731 TGGGGCTGCTGGACAGATGGCGCTCTGGCTGGGTGCGAGGAGACATCGAGCCTTC 790  
DB 628 TGGGGTCACTTGGACAGGTGGCTGCACTACGCTGGGTCCAGGACAACTTCCCACTTT 687  
QY 911 ACCGGTTATTACAGACTTTTTCATCACTAGTAGTAACCCACTGAAAGTGGCCAGAGGTGGCC 970  
DB 808 GTGTCCCTCAGCTGCTCTGATTACACAGATGTAAAGCCCATGTGCTGGTGGTTC 867  
QY 971 CACTGGGTGATGCAACCAACAGCAGACAGATCTCTGTAACCTGCTGAGGGCACTA 1030  
DB 868 ACTCTTTCTGGGTGTAATAACTACCACTCAGCTGTATGGTTTTCATTTGCTGCGCAGAG 927  
QY 1031 TCAGGGACCAAGGTGATCGGTGTGCCAACAGATGAGATTCCTCCAACTGAACCTTCAG 1090  
DB 928 ACAGAGGATGAACACTACTGAGACCTCACTAAATTTGAATCTTTTAACTGCACTTACT 987  
QY 1091 AGAGACCCGGGAGAGATTATCTGGTCCATGAGCCCTGTGGTGGATGGTGTGGTATCCCA 1150  
DB 988 GGAATCCAAAGAGAGCTATCCCTCTCTCTCTGATTGATGATGAGTAGTTCGTCCA 1047  
QY 1151 GATGACCTTTGGTCTCTGACCCAGCGGAGGTTTTCATCTGTGCCCTACCTCTAGT 1210  
DB 1048 AAGGCACAGAGAGATCTGGCTGAGAAGAGTTTCAGCACTGTCCCTACATAGTGGC 1107  
QY 1211 GTCAACAACTGGAATTCAAATGGCTCTTGGCTTATATCATGAAGTTCCTCGCTAAACCGG 1270  
DB 1108 ATCAACAGCAAGAGTTTGGCTGGATCATTCACACGCTTATGGGCTATCCACTCGCTGAA 1167  
QY 1271 CAGGCGATGAGAAAGAAACCATCATAGATGCTCTGAGTACCGGACCCCTGTGTGAT 1330  
DB 1168 GGCAAACTGGACAGAGACAGCCAAATCTCTCTTGTGGAAGTCTCTCCCAACACTTAAA 1227  
QY 1331 ATCAACAGGAGCAGGTACCACTTGTGGTGGAGGAGTACCTGGAACAATGTCAATGAGCAT 1390  
DB 1228 ATCTGAGAAATATGATTCAGTGTGCTGAGAGATTTTAGGAGGAGCAGATGACCTC 1287  
QY 1391 GACTGGAAGATCTACGAAACCGTATGATGAGCATAGTTTCAAGATGCCACTTTTCGTGTAT 1450  
DB 1288 ACCAAAAAGA-----AGACCTGTTCCAGGACTTGTGGTGTGATGTGTGTGTC 1341  
QY 1451 GCCACACTGCAGACTGCTCACTACACCGAGATGCCGCCCTCCCTGCTTACCTGTATGAA 1510  
DB 1342 CCATCAGTATTTGTCTGAAAGTACAGAGATGTGGAGCCTCCACCTATATGATGAG 1401  
QY 1511 TTTGAGCACACGCTCG---TGAATAATTCGTCAAAACCCCGCACTGATGGGAGACCAT 1567  
DB 1402 TTTGAGTATCGCCCAAGCTTTGTATCGGCCATGAGACCCAGGAGAGTAATAGGAGACCAT 1461  
QY 1568 GGGGATGAGATGTACTTCTCTTTGGGGGCCCCCTTCGCCACAGGCTTTTCCATGGGTAG 1627



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RESULT 11
AA450272      403 bp      mRNA      linear      EST 04-JUN-1997
LOCUS      Zx42H02.r1 Soares_total_fetus Kb2Hf8.9w Homo sapiens cDNA clone
DEFINITION      IMAGE:789171 5' similar to IR:G1931 G1931 CARBOXYLESTERASE
PRECUSOR      ; mRNA sequence.
ACCESSION      AA450272
VERSION      AA450272
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 403)
AUTHORS      Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Scheinberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
TITLE      WashU-Merck EST Project 1997
JOURNAL      Unpublished (1997)
COMMENT      Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES
     source
     1..403
         /organism="Homo sapiens"
         /mol_type="mRNA"
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         /lab_host="DH10B"
         /clone_lib="Soares total fetus Nb2Hf8.9w"
         /notes="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - Cligo(dR) primer [5',
TGTTACCAATGTAAGTGGGCGCGCTTAATTTTATTTTATTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p773 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bonaldo."
ORIGIN
     Query Match      18.3%; Score 363.8; DB 9; Length 403;
     Best Local Similarity 97.7%; Pred. No. 1.4e-74;
     Matches 390; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
QY      858 TGATGTCAACCCCTAGCCTCGGGTCTCTTCCATCGGGCCATTCGCCAGTGGCAACCCCGT 917
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QY      918 TATTACAGCTTTTCATCTACCTAGTAAACCACTGAAGTGGCCAGAAAGTTGCCACCTGG 977
DB      61 TGTTACAGCTTTTCATCTACCTAGTAAACCACTGAAGT-GCCAAAGAGTTGCCACCTGG 119
QY      978 CTGGATGCAACCAACACAGCACACAGATCTCTGGTAAACTGCTGAGGGCACTATCAGGGA 1037
DB      120 CTGGATGCAACCAACACAGCACACAGATCTCTGGTAAACTGCTGA-GGCACTATCAGGGA 178
QY      1038 CCAGGTGATCGGTGTGTCACCAAGATGAGATTCCTCCAACTGAACTTCAGAGAGACC 1097
DB      179 CCAGGTGATCGGTGTGTCACCAAGATGAGATTCCTCCAACTGAACTTCAGAGAGACC 238
QY      1098 CGGAAGAGATTATCTGGTCCATGAGCCCTGPGTGGATGGTGGTGGTATCCAGATGACC 1157

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Db      239 CGGAAGAGATTATCTGGTCCAAGGCCCTGTGTGGATGGTGGTGGTATCCAGATGACC 298
QY      1158 CTTTGGTCTCTCTGACCCAGGGGAAGGTTTCATCTGTGCCCCCTACCTTCTAGTGTCAACA 1217
Db      299 CTTTGGTCTCTCTGACCCAGGGGAAGGTTTCATCTGTGCCCCCTACCTTCTAGTGTCAACA 358
QY      1218 ACCTGGAATTCGAATGGCTCTTGTCTTATATCATGAAGT 1256
Db      359 ACCTGGAATTCGAATGGCTCTTGTCTTATGAAGTGAGT 397

RESULT 12
CF116765      478 bp      mRNA      linear      EST 23-JUL-2003
LOCUS      ad555.z1 ad adult sheep skin library Ovis aries cDNA, mRNA
DEFINITION      sequence.
ACCESSION      CF116765
VERSION      CF116765.1 GI:33179023
KEYWORDS      EST.
SOURCE      Ovis aries (sheep)
ORGANISM      Ovis aries
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Caprinae; Ovis.
REFERENCE      1 (bases 1 to 478)
AUTHORS      Desilva,U., Franklin,I.R., Maddox,J.F., van Hest,B. and
Adelson,D.L.
TITLE      Gene Expression in Sheep Skin and Wool (Hair)
JOURNAL      Cytogenet. Genome Res. (2003) In press
COMMENT      Contact: David L. Adelson
Animal Breeding and Genetics
Texas A&M University
Animal Science Dept., TAMU-2471, College Station, TX 77843-2471,
USA
Tel: 9798452616
Fax: 9798456970
Email: david.adelson@tamu.edu.
FEATURES
     source
     1..478
         /organism="Ovis aries"
         /mol_type="mRNA"
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         /db_xref="taxon:9940"
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         /dev_stage="Adult"
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         /clone_lib="ad adult sheep skin library"
         /note="Organ: midflank skin; Vector: pTriplex; Site 1:
EcoRI; Site 2: XbaI; Arrayed library filters screened by
hybridization with labeled dinucleotide repeats. first
strand synthesis XbaI-(dR)15 primed, EcoRI adaptors were
ligated to cDNA before cloning. EcoRI- NotI- SalI adaptor
sequence; 5'-AATTTCGGCGCGCTCGAC GCGCGGCGAGCTG-P04-5' 5'
sequencing primer 5' TCGAGATCTGGAGAGC 3' 3' sequencing
primer 5' TATACGACTCACTATAGG 3' submitted sequences in
excess of 50 bp after vector and quality clipping(phred
13) submitted to GenBank."
ORIGIN
     Query Match      17.5%; Score 346.6; DB 14; Length 478;
     Best Local Similarity 84.1%; Pred. No. 1.7e-70;
     Matches 391; Conservative 0; Mismatches 74; Indels 0; Gaps 0;
QY      307 CATCAAGTCCTTTTAGGAGTCCCTTCTCCAGACTCTCTTAGTATCTCTAGGTTTGC 366
DB      14 CATCAATGTCCTCTAGGAGTTCCTCTCCAGACTCTCTTAGTATCTCTAGGTTTGC 73
QY      367 ACCTCCAGAACCCCGGAGCCCTGGAAGGAATCAGATGTACACCTACCCCTGG 426
DB      74 TGCCCCAGAACCCCGGAGCCCTGGAAGGAATCAGATGTACACCTATGCCCTGT 133
QY      427 GTGCCCTGCAAGGAGTCTGGGGCCAGCTGGCTTCGATGTACGTACAGCCGGGAACGTA 486

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Db 134 GTGGCTCAGAGAGTCCTGGGGGAGGTCACCTCCATCTATTTCACACACGCGAGCGATA 193

Qy 487 CAAGTGGCTGGCTTACGAGGAGTCTCTGTACTGAACGTGTACGCGCGGCGCGCGC 546

Db 194 TAAATGGCTGCACCTCAATGAGGAGTCTGTACTGAATGTGCACGCGCCAGTGGGAGC 253

Qy 547 GCGCGGGATCCAGCTGCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 606

Db 254 GCGCGGGAGCCCTCTGAGCGCGGTGATCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 313

Qy 607 CGCTGCTCTTCTGTCACAGGAGCTCTGACTTGGCGCGCGCGCGAGAAAGTGTGTGTGT 666

Db 314 TTCCGCTTCCAGGTACGATGGCTCCGATTTGGCTGCGCGCGGAGAAAGTGTGTGTGT 373

Qy 667 TCTGACGACAGGCTCGGATCTTTCGGCTTCTGAGCAGGACGACGACGCGCGCGG 726

Db 374 TCTGACGACAGGCTCGGATCTTTCGGCTTCTGAGCAGGACGACGACGCGCGCGG 433

Qy 727 GAACTGGGGGCTGTGACACAGATGGCGGCTCTGCGCTGGTGCA 771

Db 434 GAACTGGGGGCTGTGACACAGATGGCGGCTCTGCGCTGGTGCA 478

RESULT 13  
LOCUS BX488287 442 bp mRNA linear EST 04-SRP-2003  
DEFINITION DKFP2686E07269 r1.686 (synonym: hlcc3) Homo sapiens cDNA clone  
similar to SW:5485.1, mRNA sequence.

ACCESSION BX488287  
VERSION BX488287.1 GI:31953725  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 442)  
Bloeker, H., Boecker, M., Mewes, H.W., Weil, B., Amid, C., Osanger, A.,  
Fobo, G., Han, M. and Wiemann, S.  
EST (Bloeker, H., Boecker, M., Mewes, H.W., Weil, B., Amid, C., et al.)  
Unpublished (2003)  
Contact: MIPS  
MIPS

TITLE Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by GBF National Research Centre for Biotechnology Ltd.,  
Braunschweig/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
No si. sequence available.  
This clone (DKFP2686E07269) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

JOURNAL Location/Qualifiers  
COMMENT 1..442  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="DKFP2686E07269"  
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/lab\_host="DH10B"  
/clone\_lib="686 (synonym: hlcc3)"  
/note="vector: pTriplex2; Site\_1: SfiIA; Site\_2: SfiIB;  
cDNA-collection"

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/mol\_type="mRNA"  
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cDNA-collection"

Query Match 17.3%; Score 343; DB 13; Length 442;  
Best Local Similarity 100.0%; Pred. No. 1.1e-69;  
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 426 GTGGCTGAGGAGTCTCGGGGCGAGTGGCTCGATGTACGTACGACGCGGGAACGGT 485

Db 100 GGTGCTGAGGAGTCTCGGGGCGAGTGGCTCGATGTACGTACGACGCGGGAACGGT 159

Qy 486 ACAAGTGGCTGGCTTACGCGAGGACTGTCTGTACTGAACGTGTACGCGCGCGCGCG 545

Db 160 ACAAGTGGCTGGCTTACGCGAGGACTGTCTGTACTGAACGTGTACGCGCGCGCGCG 219

Qy 546 GCGCGGGGATCCAGCTGCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 605

Db 220 GCGCGGGGATCCAGCTGCCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 279

Qy 606 GCGTGTCTTCTTCTGTCACAGGAGCTCTGACTTGGCGCGCGCGAGAAAGTGTGTGTGT 665

Db 280 GCGTGTCTTCTTCTGTCACAGGAGCTCTGACTTGGCGCGCGCGAGAAAGTGTGTGTGT 339

Qy 666 TTCTGACGACAGGCTCGGATCTTTCGGCTTCTGAGCAGGACGACGACGCGCGCGG 725

Db 340 TTCTGACGACAGGCTCGGATCTTTCGGCTTCTGAGCAGGACGACGACGCGCGCGG 399

Qy 726 GAACTGGGGGCTGTGACACAGATGGCGGCTCTGCGCTGGT 768

Db 400 GAACTGGGGGCTGTGACACAGATGGCGGCTCTGCGCTGGT 442

RESULT 14  
LOCUS AI949486 438 bp mRNA linear EST 08-MAR-2000  
DEFINITION wq10h04.x1 NCI CGAP Kid12 Homo sapiens cDNA clone IMAGE:2470903 3'  
similar to SW:SASB\_ANAPL\_Q04791 FATTY ACYL-CoA HYDROLASE PRECURSOR,  
MEDIUM CHAIN ;, mRNA sequence.

ACCESSION AI949486  
VERSION AI949486.1 GI:5741718  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 438)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: CGAPBS-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
Insert Length: 498 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 330.

JOURNAL Location/Qualifiers  
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/note="Torgan: kidney; Vector: p7T3D-Pac (Pharmacia) with  
a modified polylinker; Site1: Not I; Site2: Eco RI;  
Plasmid DNA from the normalized library NCI-CGAP Kids was  
prepared, and ss circles were made in vitro. Following HAP  
purification, this DNA was used as tracer in a subtractive  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(cloneIDs 1323912-1325831, 1471368-1472903 and  
1492104-1493255). Subtraction by Bento Soares and M.  
Fatima Bonaldo."

FEATURES  
source  
1..438  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2470903"  
/tissue\_type="2 pooled tumors (clear cell type)"  
/lab\_host="DH10B"  
/clone\_lib="NCI-CGAP\_Kid12"  
/note="Torgan: kidney; Vector: p7T3D-Pac (Pharmacia) with  
a modified polylinker; Site1: Not I; Site2: Eco RI;  
Plasmid DNA from the normalized library NCI-CGAP Kids was  
prepared, and ss circles were made in vitro. Following HAP  
purification, this DNA was used as tracer in a subtractive  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(cloneIDs 1323912-1325831, 1471368-1472903 and  
1492104-1493255). Subtraction by Bento Soares and M.  
Fatima Bonaldo."

ORIGIN

Query Match	16.7%; Score 331.6; DB 9; Length 438;
Best Local Similarity	98.8%; Pred. No. 5.4e-67;
Matches 334; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
Qy	89 ACGGCTACCATGCCATCCACAGTGTGCGATTCACAGTGTTGCATCCTGCTGCCACA 148 
Dd	434 ACGGCTACCATGCCATCCACAGTGTGCGATTCACAGTGTTGCATCCTGCTGCCACA 375 
Qy	149 GCAGGAGCTGGCTGGAGCATGAGTGGAATCTGTGCTGGAGGCTCACCTCTGCGCTGATG 208 
Dd	374 ACAGGAGCTGGCTGGAGCATGAGTGGAATCTGTGCTGGAGGCTCACCTCTTGGCTGATG 315 
Qy	209 GCGCAGACGGCTTTGGTGTCCTTGCACACCAAGAGGCTCAAGTGGTCACCAAATATGGA 268 
Dd	314 GCGCAGACGGCTTTGGTGTCCTTGCACACCAAGAGGCTCAAGTGGTCACCAAATATGGA 255 
Qy	269 ACCCTGCAAGGAAAAACAGATGCATGTGGGGAAAGACACCATCCCAAGTCTTTTTTAGGATC 328 
Dd	254 ACCCTGCAAGGAAAAACAGATGCATGTGGGGAAAGACACCCATCCAAGTCTTTTTTAGGATC 195 
Qy	329 CCCTTCTCCAGACCTCCTCTAGGTATCCTCAGGTTTGCACTCCAGAACCCTCCGGAGCCC 388 
Dd	194 CCCTTCTCCAGACCTCCTTTAGGTATCCTCAGGTTTGCACTCCAGAACCCTCCGGAGCCC 135 
Qy	389 TGGAAAAGGAATCAGAGATGCTTACCACCTACCCGGCTGG 426 
Dd	134 TGGAAAAGGAATCAGAGATGCTTACCACCTTACCCGGCTGG 97 
RESULT 15	
BX336837	
LOCUS	884 bp mRNA linear EST 01-MAY-2003
DEFINITION	BX336837 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODIO3YE23 5-PRIME, mRNA sequence.

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BX336837      884 bp      mRNA      linear      EST 01-MAY-2003
BX336837 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI033YE23 5-PRIME, mRNA sequence.

ACCESSION      BX336837
VERSION
KEYWORDS
SOURCE
ORGANISM      Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 884)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqres@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8153.f.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue Genoscope sequence ID : CSODI033AC12Q91.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI033YE23"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-cligo(drf)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
FEATURES
source

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ORIGIN	Query Match	16.1%	Score 320;	DB 13;	Length 884;
	Best Local Similarity	84.7%	Pred. No. 4.5e-64;		
	Matches 403; Conservative	0;	Mismatches	0;	Indels 73; Gaps 1;

QY	1477	CCGAGATGCGGGCTCCCTGCTACCTGTATGAATTTGAGCACCAAGCTCGTGGATAAT	1536
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QY	1537	CGTCAAAACCCGCACTGATGGGCGAGACCATGGGATGAGATCTCTCTTTGGGG	1596
DB	169	CGTCAAAACCCGCACTGATGGGCGAGACCATGGGATGAGATCTCTCTTTGGGG	228
QY	1597	CCCCTTCGCACAGGCCCTTTCCATGGGTAGGAGAGGCACTTAGCGCTCAGATGATGA	1656
DB	229	CCCCTTCGCACA-----	241
QY	1657	ATACTGGGCCAACTTTGCCCGCACAGAGAACCCCAATGATGGCAATCTGCCCTGCTGGCC	1716
DB	242	-----GAACCCCAATGATGGCAATCTGCCCTGCTGGCC	275
QY	1717	ACGCTACAACAAGGATGAAAAGTACTGTCAGCTGGATTTTACACAAGAGTGGGCATGA	1776
DB	276	ACGCTACAACAAGGATGAAAAGTACTGTCAGCTGGATTTTACACAAGAGTGGGCATGA	335
QY	1777	GCTCAAGGAGAAGATGGCTTTTGGATGATCTGTACAGCTCTCAAGACCTCAGAA	1836
DB	336	GCTCAAGGAGAAGATGGCTTTTGGATGATCTGTACAGCTCTCAAGACCTCAGAA	395
QY	1837	GCAGAGCAATTTCTAAGGGTGGGTATGCAGAGAGGAGCCAAAGAGGGGTTTGCCCCACC	1896
DB	396	GCAGAGCAATTTCTAAGGGTGGGTATGCAGAGAGGAGCCAAAGAGGGTTTGCCCCACC	455
QY	1897	ATCCAGGCCCTGGGAGACTAGCCATGGACATACCTGGGGACAAGAGTCTTACCCA	1952
DB	456	ATCCAGGCCCTGGGAGACTAGCCATGGACATACCTGGGGACAAGAGTCTTACCCA	511

Search completed: August 11, 2004, 18:13:28  
Job time : 5231.08 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2004, 22:23:05 ; Search time 57 Seconds

(without alignments)  
2894.873 Million cell updates/sec

Title: US-10-001-227-2

Perfect score: 3112  
Sequence: 1 MPSTVLSTVLPSSLPTAGA.....KMAFWMSLYQSQRPEKQRF 584

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_29Jan04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1980s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3112	100.0	584	5	ABb79484 Human car
2	3112	100.0	584	5	Aae21052 Human dru
3	2391.5	76.8	509	4	Abg10635 Novel hum
4	2026.5	65.1	545	2	Aay41723 Human PRO
5	2026.5	65.1	545	4	Aau29052 Human PRO
6	2026.5	65.1	545	6	Abu58428 Human PRO
7	2026.5	65.1	545	6	Abu87976 Novel hum
8	2026.5	65.1	545	6	Abu84291 Human sec
9	2026.5	65.1	545	6	Abf66165 Human sec
10	2026.5	65.1	545	6	Abf65555 Human sec
11	2026.5	65.1	545	6	Abu99495 Human sec
12	2026.5	65.1	545	6	Abu82734 Human PRO
13	2026.5	65.1	545	6	Abu89855 Novel hum
14	2026.5	65.1	545	6	Abf68104 Human sec
15	2026.5	65.1	545	6	Abu96157 Novel hum
16	2026.5	65.1	545	6	Abu92588 Human sec
17	2026.5	65.1	545	6	Abc08665 Human sec
18	2026.5	65.1	545	6	Abc02717 Human sec
19	2026.5	65.1	545	6	Abf74871 Human sec
20	2026.5	65.1	545	6	Abf94633 Human sec
21	2026.5	65.1	545	6	Abc025225 Novel hum
22	2026.5	65.1	545	6	Abu85606 Human PRO
23	2026.5	65.1	545	6	Abu98766 Novel hum
24	2026.5	65.1	545	6	Abu97981 Novel hum
25	2026.5	65.1	545	6	Abu91687 Novel hum

26	2026.5	65.1	545	6	ABU72231	Novel hum
27	2026.5	65.1	545	6	ABU89380	Human PRO
28	2026.5	65.1	545	6	ABU86221	Human sec
29	2026.5	65.1	545	6	ABU67434	Human sec
30	2026.5	65.1	545	6	ABU80462	Human PRO
31	2026.5	65.1	545	6	ABR99380	Human sec
32	2026.5	65.1	545	6	ABR98770	Human sec
33	2026.5	65.1	545	6	ABO16293	Human sec
34	2026.5	65.1	545	6	ABR92193	Human sec
35	2026.5	65.1	545	6	ABO18834	Human sec
36	2026.5	65.1	545	6	ABR78255	Human sec
37	2026.5	65.1	545	6	ABU84991	Novel hum
38	2026.5	65.1	545	6	ABO00130	Novel hum
39	2026.5	65.1	545	6	ABO11462	Human sec
40	2026.5	65.1	545	6	ABO02107	Human sec
41	2026.5	65.1	545	6	ABU88681	Novel hum
42	2026.5	65.1	545	6	ABU83376	Human sec
43	2026.5	65.1	545	6	ABO06177	Novel hum
44	2026.5	65.1	545	6	ABR59213	Human sec
45	2026.5	65.1	545	6	ABO09275	Human sec

## ALIGNMENTS

RESULT 1  
ABb79484  
ID ABB79484 standard; protein; 584 AA.  
XX  
AC ABB79484;  
XX  
DT 23-SEP-2002 (first entry)  
XX  
DE Human carboxylesterase-2 (COE-2).  
XX  
KW Carboxylesterase-2; COE-2; human; antiinflammatory; virucide; antiulcer;  
antiasthmatic; antirheumatic; antiarthritic; dermatological;  
KW antipsoriatic; analgesic; antitumour; cytostatic; enzyme; gene therapy.  
XX  
OS Homo sapiens.

XX	Key	Location/Qualifiers
FT	Domain	25..569
FT		/note= "Carboxylesterase domain"
FT	Domain	26..45
FT		/note= "Transmembrane domain"
FT	Domain	44..158
FT		/note= "type-B similar family carboxylesterase/ lipase domain"
FT	Domain	52..115
FT		/note= "carboxylesterase precursor domain"
FT	Region	137..147
FT		/note= "Carboxylesterase type B2 signature motif"
FT	Domain	144..246
FT		/note= "hydrolase lipase hormone-sensitive lipid degradation domain"
FT	Region	231..246
FT		/note= "Carboxylesterase type B1 signature motif"
FT	Domain	245..263
FT		/note= "Transmembrane domain"
FT	Domain	249..308
FT		/note= "type-B similar family carboxylesterase/ lipase domain"
FT	Domain	254..340
FT		/note= "Carboxylesterase family multigene reticulum hydrolase signal domain"
FT	Domain	254..332
FT		/note= "Glycoprotein serine carboxylesterase acetylcholinesterase cocaine B-esterase domain"
FT	Domain	360..542
FT		/note= "Esterase hydrolase p-nitrobenzyl polyurethane domain"
FT	Domain	364..577





FT Protein 44..584  
 FT /note= "Mature human DME-10 protein"  
 FT Domain 137..147  
 FT /note= "Carboxylesterase B2 motif"  
 FT Domain 231..246  
 FT /note= "Carboxylesterase B1 motif"  
 XX WO200212467-A2.  
 XX 14-FEB-2002.  
 XX 03-AUG-2001; 2001WO-US024382.  
 XX 04-AUG-2000; 2000US-0223055P.  
 XX 11-AUG-2000; 2000US-0224728P.  
 XX 18-AUG-2000; 2000US-0226440P.  
 XX 24-AUG-2000; 2000US-0228067P.  
 XX 31-AUG-2000; 2000US-0230063P.  
 XX 13-SEP-2000; 2000US-0232244P.  
 XX 20-SEP-2000; 2000US-0234269P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX Baughn MR, Bruns CM, Das D, Delegeane AM, Ding L, Elliot VS;  
 PI Gandhi AR, Griffin JA, Hafalia AJA, Khan FA, Lal P, Lee S, Lu DAM;  
 PI Lu Y, Patterson C, Ramkumar J, Ring HZ, Sanjanwala MS, Tang YT;  
 PI Thangavelu K, Thornton M, Tribouley CM, Walla NK, Warren BA, Yang J;  
 PI Yao MG, Yue H;  
 XX WPI; 2002-206331/26.  
 XX N-PSDB; AAD33489.  
 XX New human drug metabolizing enzyme polypeptide and polynucleotide useful  
 PT for diagnosing, treating and preventing cell proliferative,  
 PT autoimmune/inflammatory, endocrine, eye, metabolic and gastrointestinal  
 PT disorders.  
 XX Claim 54; Page 154-156; 179pp; English.  
 XX The invention relates to an isolated human drug metabolising enzyme (DME)  
 CC polypeptide or a biologically active or immunogenic fragment of DME. DME  
 CC is useful for diagnosis, treatment and prevention of cell proliferative,  
 CC autoimmune/inflammatory, developmental, endocrine, eye, metabolic and  
 CC gastrointestinal disorders including live disorders. Autoimmune/  
 CC inflammatory disorders include acquired immunodeficiency syndrome (AIDS),  
 CC adult respiratory distress syndrome, Addison's disease, atherosclerosis,  
 CC allergies, anaemia, asthma, autoimmune haemolytic anaemia, autoimmune  
 CC thyroiditis, Crohn's disease, atopic dermatitis, diabetes mellitus,  
 CC glomerulonephritis, rheumatoid arthritis, systemic lupus erythematosus,  
 CC ulcerative colitis, uveitis, viral, bacterial, protozoal, parasitic,  
 CC fungal, helminthic infections and trauma. Cell proliferative disorders  
 CC include cancer, arteriosclerosis, cirrhosis and psoriasis; developmental  
 CC disorders include epilepsy and cataract; and endocrine disorders include  
 CC disorders of hypothalamus/pituitary, disorders associated with  
 CC hypopituitarism, including diabetes insipidus, hypogonadism, disorders  
 CC associated with hypothyroidism including goitre, Grave's disease,  
 CC pancreatic disorders such as diabetes mellitus, disorders associated with  
 CC adrenals, disorders associated with gonadal steroid hormones such as  
 CC endometriosis, infertility, hypergonadal disorders and gynaecomastia.  
 CC Disorders of the eye include conjunctivitis and macular degeneration and  
 CC metabolic disorders include diabetes, cystic fibrosis, obesity and  
 CC hypocalcaemia. Gastrointestinal disorders include gastritis, peptic  
 CC ulcer, hepatitis, constipation, diarrhoea, jaundice, Wilson's disease,  
 CC thrombosis and hepatic tumours. DME gene is useful in gene therapy. The  
 CC present sequence is human DME-10 protein  
 XX Sequence 584 AA;

Query Match 100.0%; Score 3112; DB 5; Length 584;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-286;  
 Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSTVLPSTVPSLLPTAGAGSMRWILCWSLTCLMAQTALGALHTKRPQVTKYGLQ 60

Db 1 MPSTVLPSTVPSLLPTAGAGSMRWILCWSLTCLMAQTALGALHTKRPQVTKYGLQ 60  
 QY 61 GQMHVGTPTQVFLGVFSPRPPIGLRFAPPEPPKGIIDATYTPFGCLQESWGQIA 120  
 Db 61 GQMHVGTPTQVFLGVFSPRPPIGLRFAPPEPPKGIIDATYTPFGCLQESWGQIA 120  
 QY 121 SMYVSTRERYKWLRFSEDCLYLVNYPAPAPGDPOLPVMVWPPGGAFIVGAASSYEGSD 180  
 Db 121 SMYVSTRERYKWLRFSEDCLYLVNYPAPAPGDPOLPVMVWPPGGAFIVGAASSYEGSD 180  
 QY 181 AAREKVLVFLQHLRIGIFGLSTDDSHARGNWGLLDQVAALRWQENIAAFGGDPGNVTL 240  
 Db 181 AAREKVLVFLQHLRIGIFGLSTDDSHARGNWGLLDQVAALRWQENIAAFGGDPGNVTL 240  
 QY 241 FQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKVAAHLACGNHS 300  
 Db 241 FQSAGAMSISGLMMSPLASGLFHRAISQSGTALFRLFITSNPLKVAKVAAHLACGNHS 300  
 QY 301 TQILVNCRLAALSGTKVNRVSNKQRFQLNFORDPDEEIIWSMSPVVDGVVIPPDDPLVLTQ 360  
 Db 301 TQILVNCRLAALSGTKVNRVSNKQRFQLNFORDPDEEIIWSMSPVVDGVVIPPDDPLVLTQ 360  
 QY 361 GKVSVPYLLGVNNLEFNNLLPYINKFPLNRQAMEKETITKWLSTRLLNITKEOVPLV 420  
 Db 361 GKVSVPYLLGVNNLEFNNLLPYINKFPLNRQAMEKETITKWLSTRLLNITKEOVPLV 420  
 QY 421 VREYLDNVNEHDWKLRNRMDIVQDATFVYATLQTAHYHRDAGLPVLYEFEEHARGII 480  
 Db 421 VREYLDNVNEHDWKLRNRMDIVQDATFVYATLQTAHYHRDAGLPVLYEFEEHARGII 480  
 QY 481 VKPRTDGADHGDEMFLFGGPPATGLSMGKEKALSQMKYKWANFARTGNPDNGLPCWP 540  
 Db 481 VKPRTDGADHGDEMFLFGGPPATGLSMGKEKALSQMKYKWANFARTGNPDNGLPCWP 540  
 QY 541 RYNKDEKYLQDLFTTRVGMKLEKKAFAWMSLYQSORPEKQRF 584  
 Db 541 RYNKDEKYLQDLFTTRVGMKLEKKAFAWMSLYQSORPEKQRF 584  
 XX RESULT 3  
 XX ABG10635  
 XX ID ABG10635 standard; protein; 509 AA.  
 XX AC ABG10635;  
 XX XX 13-FEB-2002 (first entry)  
 XX DE Novel human diagnostic protein #10626.  
 XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 XX KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX OS Homo sapiens.  
 XX WO200175067-A2.  
 XX XX 11-OCT-2001.  
 XX XX 30-MAR-2001; 2001WO-US008631.  
 XX PF 31-MAR-2000; 2000US-00540217.  
 XX PR 23-AUG-2000; 2000US-00649167.  
 XX XX (HYSE-) HYSEQ INC.  
 XX XX Drmanac RT, Liu C, Tang YT;  
 XX WPI; 2001-639362/73.  
 XX DR N-PSDB; AAS74822.  
 XX XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensic, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.

XX Claim 20; SEQ ID NO 40994; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, CC and in recombinant production of (II). The polynucleotides are also used CC in diagnostics as expressed sequence tags for identifying expressed CC genes. (I) is useful in gene therapy techniques to restore normal CC activity of (II) or to treat disease states involving (II). (II) is CC useful for generating antibodies against it, detecting or quantitating a CC polypeptide in tissue, as molecular weight markers and as a food CC supplement. (II) and its binding partners are useful in medical imaging CC of sites expressing (II). (I) and (II) are useful for treating disorders CC involving aberrant protein expression or biological activity. The CC polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations CC and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ASG30377 represent novel human diagnostic CC amino acid sequences of the invention. Note: The sequence data for this CC patent did not appear in the printed specification, but was obtained in CC electronic format directly from WIPO at CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 509 AA;

Query Match 76.8%; Score 2391.5; DB 4; Length 509;

Best Local Similarity 90.9%; Pred. No. 5e-218;

Matches 461; Conservative 2; Mismatches 13; Indels 31; Gaps 3;

QY	103	PG---CCQESWGQASMTVSTRERYKMLRFSEDCLYLVNVPAPAPAGDPDPVWVFPFGG	165
DB	3	FGARCLHEFWGQASMTVSTRERYKMLRFNEDCLYLVNVPAPAPAGDPDPVWVFPFGG	62
QY	166	AFIVGAASSYSGSLAAREKVLVFLQHRGIFGLSTDSDHARGNGLDQMAALRWVQ	225
DB	63	AFIVGAASSYSGSLAAREKGLVFLQHRGIFGLSTDSDHARGNGLDQMAALRWVQ	122
QY	226	ENIAAFGDPGCV--TLFGQSAGVSIQGLWMSPLASGLFHRAISQGTALFRFLFITSNPL	284
DB	123	ENIAAFGRPREIITLFGQSAGVSIQGLWMSPLASGLFHRAISQGTALFRFLFITSNPL	182
QY	285	KVAKKVAHLACGNHNSQIILVNCILRALSGTKVMKRVSNKMRFLQINFORDPPEIISWSPV	344
DB	183	KVAKKVAHLACGNHNSQIILVNCILRALTRAKVMKRVSNKMRFLQINFORDPPEIISWSPV	242
QY	345	VDGVIPDDPLVLTQGVSSVPVLLGVNLEFNLLPYIMKPLNRAQMKETITKMLW	404
DB	243	VDGVIPDDPLVLTQGVSSVPVLLGVNLEFNLLPYIMKPLNRAQMKETITKMLW	302
QY	405	STRTLL-----NITKEQVPLVVEEYLDNVNNEHDKMLR	437
DB	303	STRTLLAKNSGABHGSLSVGPPLAQLAPRPNITKEQVPLVVEEYLDNVNNEHDKMLR	362
QY	438	NRWMDIVODATFVATQTAHYHHDAGLVPVLYFEFHARGIIVKPTDGDHGDWYFL	497
DB	363	NRWMDIVODATFVATQTAHYHHDAGLVPVLYFEFHARGIIVKPTDGDHGDWYFL	422
QY	498	FGGPFATGLSGKEKALSQWKYKWFANFARTGNPDGNLPCWPRYNKDEKYLQLDFTTRV	557
DB	423	FGGPFATGLSGKEKALSQWKYKWFANFARTGNPDGNLPCWPRYNKDEKYLQLDFTTRV	482
QY	558	GNKLEKKEKMAFWMSLYSQRPKQRF	584
DB	483	GNKLEKKEKMAFWMSLYSQRPKQRF	509

RESULT 4

RAY41723

ID RAY41723 standard; protein; 545 AA.

XX AC RAY41723;  
XX DT 07-DEC-1999 (first entry)  
XX DE Human PRO873 protein sequence.  
XX KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;  
XX KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
XX KW secreted protein; transmembrane protein.  
XX OS Homo sapiens.  
XX PN WO9946281-A2.  
XX PD 16-SEP-1999.  
XX PF 08-MAR-1999; 99WO-US005028.  
XX PR 10-MAR-1998; 98US-0077450P.  
XX PR 11-MAR-1998; 98US-0077632P.  
XX PR 11-MAR-1998; 98US-0077641P.  
XX PR 11-MAR-1998; 98US-0077649P.  
XX PR 12-MAR-1998; 98US-0077791P.  
XX PR 13-MAR-1998; 98US-0078004P.  
XX PR 17-MAR-1998; 98US-00040220.  
XX PR 20-MAR-1998; 98US-0078886P.  
XX PR 20-MAR-1998; 98US-0078910P.  
XX PR 20-MAR-1998; 98US-0078936P.  
XX PR 20-MAR-1998; 98US-0078939P.  
XX PR 25-MAR-1998; 98US-0079234P.  
XX PR 26-MAR-1998; 98US-0079656P.  
XX PR 27-MAR-1998; 98US-0079663P.  
XX PR 27-MAR-1998; 98US-0079664P.  
XX PR 27-MAR-1998; 98US-0079689P.  
XX PR 27-MAR-1998; 98US-0079728P.  
XX PR 27-MAR-1998; 98US-0079786P.  
XX PR 30-MAR-1998; 98US-0079920P.  
XX PR 30-MAR-1998; 98US-0079923P.  
XX PR 31-MAR-1998; 98US-0080105P.  
XX PR 31-MAR-1998; 98US-0080107P.  
XX PR 31-MAR-1998; 98US-0080165P.  
XX PR 31-MAR-1998; 98US-0080194P.  
XX PR 01-APR-1998; 98US-0080327P.  
XX PR 01-APR-1998; 98US-0080328P.  
XX PR 01-APR-1998; 98US-0080333P.  
XX PR 01-APR-1998; 98US-0080334P.  
XX PR 08-APR-1998; 98US-0081049P.  
XX PR 08-APR-1998; 98US-0081070P.  
XX PR 08-APR-1998; 98US-0081071P.  
XX PR 09-APR-1998; 98US-0081195P.  
XX PR 09-APR-1998; 98US-0081203P.  
XX PR 09-APR-1998; 98US-0081229P.  
XX PR 15-APR-1998; 98US-0081817P.  
XX PR 15-APR-1998; 98US-0081838P.  
XX PR 15-APR-1998; 98US-0081952P.  
XX PR 15-APR-1998; 98US-0081955P.  
XX PR 21-APR-1998; 98US-0082568P.  
XX PR 21-APR-1998; 98US-0082569P.  
XX PR 22-APR-1998; 98US-0082700P.  
XX PR 22-APR-1998; 98US-0082704P.  
XX PR 23-APR-1998; 98US-0082804P.  
XX PR 23-APR-1998; 98US-0082767P.  
XX PR 27-APR-1998; 98US-0082796P.  
XX PR 28-APR-1998; 98US-0083336P.  
XX PR 28-APR-1998; 98US-0083322P.  
XX PR 29-APR-1998; 98US-0083392P.  
XX PR 29-APR-1998; 98US-0083495P.  
XX PR 29-APR-1998; 98US-0083496P.  
XX PR 29-APR-1998; 98US-0083499P.  
XX PR 29-APR-1998; 98US-0083500P.  
XX PR 29-APR-1998; 98US-0083545P.  
XX PR 29-APR-1998; 98US-0083554P.

PR	29-APR-1998;	98US-0083558P.	QY	111	-----CLOESWGOLASMYSTRERYKWLRFSEDCLYLNV	145
PR	29-APR-1998;	98US-0083559P.	Db	167		226
PR	30-APR-1998;	98US-0083742P.	QY	146	APARAPGDPOLPVMMVPPGAFIVGAASSYEGSDLAAREKVVLFLOHRLGIFGFLSTDD	205
PR	05-MAY-1998;	98US-0084366P.	Db	227	APARAPGDPOLPVMMVPPGAFIVGAASSYEGSDLAAREKVVLFLOHRLGIFGFLSTDD	286
PR	06-MAY-1998;	98US-0084414P.	QY	206	SHARGNWGLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR	265
PR	06-MAY-1998;	98US-0084441P.	Db	287	SHARGNWGLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR	346
PR	07-MAY-1998;	98US-0084598P.	QY	266	AISQSGTALFRLFITSNPLKVAKKVAHLACNNHSTOILVNCRLALSGTKVMRVSNQRF	325
PR	07-MAY-1998;	98US-0084600P.	Db	347	AISQSGTALFRLFITSNPLKVAKKVAHLACNNHSTOILVNCRLALSGTKVMRVSNQRF	406
PR	07-MAY-1998;	98US-0084627P.	QY	326	LQINFORDDPEEIIWMSPPVVDGVIPDDPLVLTQGVKSSVPYLLGVNNLEFNWLLPYIM	385
PR	07-MAY-1998;	98US-0084637P.	Db	407	LQINFORDDPEEIIWMSPPVVDGVIPDDPLVLTQGVKSSVPYLLGVNNLEFNWLLPY--	464
PR	07-MAY-1998;	98US-0084639P.	QY	386	KFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDKMLNRMDIVQ	445
PR	07-MAY-1998;	98US-0084640P.	Db	465	-----NITKEQVPLVVEEYLDNVNEHDKMLNRMDIVQ	499
PR	07-MAY-1998;	98US-0084643P.	QY	446	DATEFYATLQTAHYHRD	462
PR	07-MAY-1998;	98US-0084643P.	Db	500	DATEFYATLQTAHYHRE	516
PR	13-MAY-1998;	98US-0085323P.	RESULT 5			
PR	13-MAY-1998;	98US-0085338P.	AAU29052			
PR	13-MAY-1998;	98US-0085339P.	ID	AAU29052	standard; protein; 545 AA.	
PR	15-MAY-1998;	98US-0085573P.	XX	AAU29052;		
PR	15-MAY-1998;	98US-0085579P.	XX	18-DEC-2001	(first entry)	
PR	15-MAY-1998;	98US-0085580P.	XX	Human PRO polypeptide sequence #29.		
PR	15-MAY-1998;	98US-0085582P.	XX	PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;		
PR	15-MAY-1998;	98US-0085697P.	XX	dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;		
PR	15-MAY-1998;	98US-0085700P.	XX	blood; chondrocyte cell; cell proliferation; cell differentiation; colon;		
PR	15-MAY-1998;	98US-0086023P.	XX	adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.		
PR	15-MAY-1998;	98US-0086392P.	XX	Homo sapiens.		
PR	22-MAY-1998;	98US-0086412P.	XX	WO200168849-A2.		
PR	22-MAY-1998;	98US-0086430P.	XX	20-SEP-2001.		
PR	22-MAY-1998;	98US-0086486P.	XX	28-FEB-2001; 2001WO-US006520.		
PR	28-MAY-1998;	98US-0087098P.	XX	01-MAR-2000; 2000WO-US005601.		
PR	28-MAY-1998;	98US-0087106P.	XX	02-MAR-2000; 2000WO-US005841.		
PR	30-JUL-1998;	98US-0094651P.	XX	03-MAR-2000; 2000US-0187202P.		
PR	11-SEP-1998;	98US-0100038P.	XX	06-MAR-2000; 2000US-0186969P.		
XX			XX	14-MAR-2000; 2000US-0189320P.		
XX			XX	14-MAR-2000; 2000US-0189328P.		
XX			XX	15-MAR-2000; 2000WO-US006884.		
XX			XX	21-MAR-2000; 2000US-0190828P.		
XX			XX	21-MAR-2000; 2000US-0191007P.		
XX			XX	21-MAR-2000; 2000US-0191048P.		
XX			XX	21-MAR-2000; 2000US-0191314P.		
XX			XX	28-MAR-2000; 2000US-0192655P.		
XX			XX	29-MAR-2000; 2000US-0193032P.		
XX			XX	29-MAR-2000; 2000US-0193053P.		
XX			XX	30-MAR-2000; 2000WO-US008439.		
XX			XX	04-APR-2000; 2000US-0194449P.		
XX			XX	04-APR-2000; 2000US-0194647P.		
XX			XX	11-APR-2000; 2000US-0195975P.		
XX			XX	11-APR-2000; 2000US-0196000P.		
XX			XX	11-APR-2000; 2000US-0196187P.		
XX			XX	11-APR-2000; 2000US-0196690P.		

29-APR-1998; 98US-0083558P.  
29-APR-1998; 98US-0083559P.  
30-APR-1998; 98US-0083742P.  
05-MAY-1998; 98US-0084366P.  
06-MAY-1998; 98US-0084414P.  
06-MAY-1998; 98US-0084441P.  
07-MAY-1998; 98US-0084598P.  
07-MAY-1998; 98US-0084600P.  
07-MAY-1998; 98US-0084627P.  
07-MAY-1998; 98US-0084637P.  
07-MAY-1998; 98US-0084639P.  
07-MAY-1998; 98US-0084640P.  
07-MAY-1998; 98US-0084643P.  
13-MAY-1998; 98US-0085323P.  
13-MAY-1998; 98US-0085338P.  
13-MAY-1998; 98US-0085339P.  
15-MAY-1998; 98US-0085573P.  
15-MAY-1998; 98US-0085579P.  
15-MAY-1998; 98US-0085580P.  
15-MAY-1998; 98US-0085582P.  
15-MAY-1998; 98US-0085697P.  
15-MAY-1998; 98US-0085700P.  
15-MAY-1998; 98US-0086023P.  
15-MAY-1998; 98US-0086392P.  
22-MAY-1998; 98US-0086412P.  
22-MAY-1998; 98US-0086430P.  
22-MAY-1998; 98US-0086486P.  
28-MAY-1998; 98US-0087098P.  
28-MAY-1998; 98US-0087106P.  
28-MAY-1998; 98US-0087208P.  
30-JUL-1998; 98US-0094651P.  
11-SEP-1998; 98US-0100038P.

(GETH ) GENENTECH INC.

Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
WPI; 1999-551358/46.  
N-PSDB; AA234105.

New secreted and transmembrane polypeptides and their polynucleotides,  
useful for treating blood coagulation disorders, cancers and cellular  
adhesion disorders.

Claim 12; Fig 91; 530pp; English.

The present invention describes secreted and transmembrane polypeptides  
and their polynucleotides. The nucleotide sequences are useful as sources  
of probes, primers, for chromosome mapping, and for generation of  
antisense sequences. They can also be used to create transgenic animals.  
The proteins can be used to treat a variety of diseases and disorders,  
depending on their function. Diseases that may be treated include blood  
coagulation disorders, cancers and cellular adhesion disorders. They may  
also be used to raise antibodies. AA233891 to AA234338, and AA41685 to  
AA41774 represent polynucleotide and polypeptide sequence given in the  
exemplification of the present invention

Sequence 545 AA;

Query Match 65.1%; Score 2026.5; DB 2; Length 545;  
Best Local Similarity 80.3%; Pred. No. 2.8e-183;  
Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

QY 6 LPSTVPSLLPTAGAGMSRWILCWSLTLCLMAQTALGALHTKRPQVVTYKTLQGMH 65  
DB 47 LGSTSTPATTAPSSGFTGLFGSKPATGFTFLGCTGNTGALHTKRPQVVTYKTLQGMH 106  
QY 66 VGKTIQVFLGVPSRPPDLILRAPPEPPPPWGTGIRDTATYPG----- 110  
DB 107 VGKTIQVFLGVPSRPPDLILRAPPEPPPPWGTGIRDTATYPGWSLALSPGMSAVARS 166

PR 11-APR-2000; 2000US-0196820P.  
 PR 18-APR-2000; 2000US-0198121P.  
 PR 18-APR-2000; 2000US-0198585P.  
 PR 25-APR-2000; 2000US-0199397P.  
 PR 25-APR-2000; 2000US-0199550P.  
 PR 25-APR-2000; 2000US-0199654P.  
 PR 03-MAY-2000; 2000US-0201516P.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 05-JUN-2000; 2000US-0209832P.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 22-AUG-2000; 2000US-00844848.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.  
 PR 20-DEC-2000; 2000WO-US034956.  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
 PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
 DR WPI; 2001-602746/68.  
 DR N-PSDB; AAS45953.  
 XX  
 PT Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
 PT presence of tumors, such as prostate and breast tumors, in mammals and to  
 PT screen for modulators of the compounds.  
 XX  
 PS Claim 11; Fig 58; 774pp; English.  
 XX  
 CC Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
 CC The PRO polypeptides and their associated nucleic acids can be used to  
 CC detect the presence of a tumour in a mammal by comparing the level of  
 CC expression of a PRO polypeptide in a test sample of cells from the animal  
 CC and a control sample of normal cells, whereby a higher level of  
 CC expression in the test sample indicates the presence of a tumour in the  
 CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
 CC and rabbits but are preferably human. The polypeptides can be used to  
 CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
 CC when contacted with it. A specific polypeptide can be used to stimulate  
 CC the proliferation or differentiation of chondrocyte cells. The PRO  
 CC proteins can be used to determine the presence of tumours and also  
 CC susceptibility to tumour development, particularly adrenal, lung, colon,  
 CC breast, prostate, cervical, or liver tumours, in mammalian  
 CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
 CC can be used for genetic analysis of individuals with genetic disorders  
 XX  
 SQ Sequence 545 AA;  
 Query Match 65.1%; Score 2026.5; DB 4; Length 545;  
 Best Local Similarity 80.3%; Pred. No. 2,8e-183;  
 Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;  
 QY 6 LPSTVPLSLPTAGAGSMRWLCLNSLTCLMAQTALGALHTKRPQVTKYTLQKQKH 65  
 DB 47 LGSTSTPATTSAPSSGFGTGLGSKPATGTLGGTNTGALHTKRPQVTKYTLQKQKH 106  
 QY 66 VGKTPIQVFLGVFPSPPLGILRFAPPEPEPWKGIRDATTYPDG-----110  
 DB 107 VGKTPIQVFLGVFPSPPLGILRFAPPEPEPWKGIRDATTYPDGNSALSPGNSAVARS 166  
 QY 111 -----CLOESWQGLASMYVSTRERYKWLRFSEDCILYLVNY 145  
 DB 167 RLATASARVQASLLPQLPSVWGYRCLOESWQGLASMYVSTRERYKWLRFSEDCILYLVNY 226  
 QY 146 APARAPDQPLPMVWFFPGATVGNASSYEGSDLAAREKVVFLQHLRIGFGLSTDD 205  
 DB 227 APARAPDQPLPMVWFFPGATVGNASSYEGSDLAAREKVVFLQHLRIGFGLSTDD 286  
 QY 206 SHARGNWGLLDQAAALRWVQENIAAFGGDPGNVTLFGQSAGAMSTISGLMSPGLASGLPFR 265

DB 287 SHARGNWGLLDQAAALRWVQENIAAFGGDPGNVTLFGQSAGAMSTISGLMSPGLASGLPFR 346  
 QY 266 AISOQGTALFLPITSNPLKVAKKVAHLACGNHNSITQILVNCRLALSGTKVMRYSNKMR 325  
 DB 347 AISOQGTALFLPITSNPLKVAKKVAHLACGNHNSITQILVNCRLALSGTKVMRYSNKMR 406  
 QY 326 LQINFRQDPPEEIIWMSMSPVWGVIPDDPLVLLTQGVKSSVPYLLGVNNEFNWLLPYIM 385  
 DB 407 LQINFRQDPPEEIIWMSMSPVWGVIPDDPLVLLTQGVKSSVPYLLGVNNEFNWLLPY-- 464  
 QY 386 KFLNLRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNNEHDMKMLRNRMMDIVQ 445  
 DB 465 -----NITKEQVPLVVEEYLDNNEHDMKMLRNRMMDIVQ 499  
 QY 446 DATFVYATLQTAHYHRD 462  
 DB 500 DATFVYATLQTAHYHRE 516  
 RESULT 6  
 ABUS8428  
 ID ABUS8428 standard; protein; 545 AA.  
 XX  
 AC ABUS8428;  
 XX  
 DT 15-APR-2003 (first entry)  
 XX  
 DE Human PRO polypeptide #29.  
 XX  
 KW Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;  
 KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;  
 KW antibody-dependent enzyme mediated prodrug therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003027272-A1.  
 PD 06-FEB-2003.  
 XX  
 PF 21-JUN-2002; 2002US-00176492.  
 PR 18-SEP-1997; 97US-0059263P.  
 PR 18-SEP-1997; 97US-0059266P.  
 PR 17-OCT-1997; 97US-0062350P.  
 PR 21-OCT-1997; 97US-0063486P.  
 PR 24-OCT-1997; 97US-0063420P.  
 PR 24-OCT-1997; 97US-0063121P.  
 PR 28-OCT-1997; 97US-0063540P.  
 PR 28-OCT-1997; 97US-0063541P.  
 PR 28-OCT-1997; 97US-0063544P.  
 PR 28-OCT-1997; 97US-0063564P.  
 PR 29-OCT-1997; 97US-0063734P.  
 PR 31-OCT-1997; 97US-0063870P.  
 PR 31-OCT-1997; 97US-0064103P.  
 PR 13-NOV-1997; 97US-0065311P.  
 PR 21-NOV-1997; 97US-0066120P.  
 PR 24-NOV-1997; 97US-0066466P.  
 PR 24-NOV-1997; 97US-0066772P.  
 PR 11-DEC-1997; 97US-0069335P.  
 PR 12-DEC-1997; 97US-0069425P.  
 PR 17-DEC-1997; 97US-0069870P.  
 PR 18-DEC-1997; 97US-0068017P.  
 PR 10-MAR-1998; 98US-0077450P.  
 PR 11-MAR-1998; 98US-0077632P.  
 PR 20-MAR-1998; 98US-0078866P.  
 PR 20-MAR-1998; 98US-0078939P.  
 PR 27-MAR-1998; 98US-0079664P.  
 PR 27-MAR-1998; 98US-0079786P.  
 PR 31-MAR-1998; 98US-0080107P.  
 PR 31-MAR-1998; 98US-0080194P.  
 PR 01-APR-1998; 98US-0080327P.







PR	10-JUN-1998;	98US-0088825P.
PR	10-JUN-1998;	98US-0088826P.
PR	11-JUN-1998;	98US-0088861P.
PR	11-JUN-1998;	98US-0088863P.
PR	11-JUN-1998;	98US-0088876P.
PR	12-JUN-1998;	98US-0089090P.
PR	12-JUN-1998;	98US-0089105P.
PR	16-JUN-1998;	98US-0089512P.
PR	16-JUN-1998;	98US-0089514P.
PR	17-JUN-1998;	98US-0089538P.
PR	17-JUN-1998;	98US-0089598P.
PR	17-JUN-1998;	98US-0089653P.
PR	18-JUN-1998;	98US-0089908P.
PR	19-JUN-1998;	98US-0089952P.
PR	22-JUN-1998;	98US-0090246P.
PR	22-JUN-1998;	98US-0090252P.
PR	22-JUN-1998;	98US-0090254P.
PR	24-JUN-1998;	98US-0090429P.
PR	24-JUN-1998;	98US-0090435P.
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PR	24-JUN-1998;	98US-0090540P.
PR	25-JUN-1998;	98US-0090676P.
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PR	25-JUN-1998;	98US-0090690P.
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PR	26-JUN-1998;	98US-009105413.
PR	26-JUN-1998;	98US-0090862P.
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PR	01-JUL-1998;	98US-0091359P.
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PR	02-JUL-1998;	98US-0091478P.
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PR	02-JUL-1998;	98US-0091626P.
PR	02-JUL-1998;	98US-0091628P.
PR	02-JUL-1998;	98US-0091632P.
PR	24-JUL-1998;	98US-0094006P.
PR	04-AUG-1998;	98US-0095282P.
PR	10-AUG-1998;	98US-0095998P.
PR	10-AUG-1998;	98US-0096012P.
PR	17-AUG-1998;	98US-0096757P.
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PR	17-AUG-1998;	98US-0096867P.
PR	17-AUG-1998;	98US-0096891P.
PR	18-AUG-1998;	98US-0096897P.
PR	18-AUG-1998;	98US-0096949P.
PR	18-AUG-1998;	98US-0096959P.
PR	18-AUG-1998;	98US-0097022P.
PR	26-AUG-1998;	98US-0097952P.
PR	26-AUG-1998;	98US-0097954P.
PR	26-AUG-1998;	98US-0097955P.
PR	26-AUG-1998;	98US-0097971P.
PR	26-AUG-1998;	98US-0097974P.
PR	26-AUG-1998;	98US-0098014P.
PR	01-SEP-1998;	98US-0098716P.
PR	01-SEP-1998;	98US-0098723P.
PR	02-SEP-1998;	98US-0098803P.
PR	02-SEP-1998;	98US-0098821P.
PR	02-SEP-1998;	98US-0098843P.
PR	09-SEP-1998;	98US-0098602P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
PR	10-SEP-1998;	98US-0099763P.
PR	10-SEP-1998;	98US-0099812P.
PR	15-SEP-1998;	98US-0100388P.
PR	16-SEP-1998;	98US-0100662P.
PR	16-SEP-1998;	98US-0100664P.
PR	16-SEP-1998;	98US-0101751P.
PR	16-SEP-1998;	98US-01008825P.
PR	17-SEP-1998;	98US-01008826P.
PR	17-SEP-1998;	98US-0100919P.
PR	17-SEP-1998;	98US-0100919P.
PR	17-SEP-1998;	98US-0100930P.
PR	18-SEP-1998;	98US-0100849P.
PR	18-SEP-1998;	98US-0101014P.
PR	18-SEP-1998;	98US-0101068P.
PR	23-SEP-1998;	98US-0101471P.
PR	23-SEP-1998;	98US-0101472P.
PR	23-SEP-1998;	98US-0101475P.
PR	23-SEP-1998;	98US-0101477P.
PR	23-SEP-1998;	98US-0101738P.
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PR	24-SEP-1998;	98US-0101743P.
PR	24-SEP-1998;	98US-0101922P.
PR	25-SEP-1998;	98US-0101786P.
PR	25-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-0102240P.
PR	29-SEP-1998;	98US-0102330P.
PR	29-SEP-1998;	98US-0102331P.
PR	30-SEP-1998;	98US-0102487P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103258P.
Query Match 65.1%; Score 2026.5; DB 6; Length 545;		
Best Local Similarity 80.3%; Pred. No. 2.8e-183;		
Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;		
QY	6 LPSTVLPSELLPTAGAGNSRWILWSLTLCLMAQTALCALHTKRPQVTKTGLGKQKH 65	
Db	47 LGSTSTPATTSAPSSGFGTGLFGSKPATGFTLGCTNTGALHTKRPQVTKTGLGKQKH 106	
QY	66 VGKTIQVFLGVFPRPPLGLIRPAPPPEPPPKWGIKIRDTATYPPG- 110	
Db	107 VGKTIQVFLGVFPRPPLGLIRPAPPPEPPPKWGIKIRDTATYPPGWSLALSPGWSAVARS 166	
QY	111 -----CLOESWGOLASMTVSTRERYKWLRFSEDCILYLVNY 145	
Db	167 RLUTATSASRVQASLLPQPLSVWGVYRCLOESWGOLASMTVSTRERYKWLRFSEDCILYLVNY 226	
QY	146 APARAPGDPQLPVMVWFFGGAFIVGAASSYEGSDLAAREKVVLFQHRIGIFGLSTDD 205	
Db	227 APARAPGDPQLPVMVWFFGGAFIVGAASSYEGSDLAAREKVVLFQHRIGIFGLSTDD 286	
QY	206 SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTILFGQSAGAMSISGLMWSPLASGLFHR 265	
Db	287 SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTILFGQSAGAMSISGLMWSPLASGLFHR 346	
QY	266 AISQSGTALFRLFITSNPLKVAKKVAHLACGNHNSITLIVNCLRALSGTKMVRVSNKMRP 325	
Db	347 AISQSGTALFRLFITSNPLKVAKKVAHLACGNHNSITLIVNCLRALSGTKMVRVSNKMRP 406	
QY	326 LQINFORDEEIIWMSPPWDGWIIPDDPLVLLTQGVSSVFFYLLGVNNLEFNWLLPYIM 385	
Db	407 LQINFORDEEIIWMSPPWDGWIIPDDPLVLLTQGVSSVFFYLLGVNNLEFNWLLPY-- 464	
QY	386 KPFLNRQAMRKETITKMLWSTLTLNITKEQVPLVVEYLDNVNHEHDKMLNRMDIVQ 445	
Db	465 -----NITKEQVPLVVEYLDNVNHEHDKMLNRMDIVQ 499	
QY	446 DATFVYATLQTAHYHRD 462	
Db	500 DATFVYATLQTAHYHRE 516	
RESULT 8		
ABU84291		
ID ABU84291 standard; protein; 545 AA.		

XX AC ABU84291; 18-MAY-1998; 98US-0086023P.  
XX AC 22-MAY-1998; 98US-0086392P.  
XX AC 22-MAY-1998; 98US-0086486P.  
XX AC 28-MAY-1998; 98US-0087098P.  
XX DE Human secreted/transmembrane protein (PRO) #29. 28-MAY-1998; 98US-0087208P.  
XX DE Human; secreted and transmembrane protein; PRO; TNF-alpha; 02-JUN-1998; 98US-0087609P.  
XX KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy; 02-JUN-1998; 98US-0087759P.  
XX KW tissue typing. 03-JUN-1998; 98US-0087827P.  
XX OS Homo sapiens. 04-JUN-1998; 98US-0088025P.  
XX PN US2003032112-A1. 04-JUN-1998; 98US-0088028P.  
XX PD 13-FEB-2003. 04-JUN-1998; 98US-0088033P.  
XX PF 21-JUN-2002; 2002US-00176756. 04-JUN-1998; 98US-0088326P.  
XX PR 18-SEP-1997; 97US-0059263P. 05-JUN-1998; 98US-0088167P.  
XX PR 18-SEP-1997; 97US-0059266P. 05-JUN-1998; 98US-0088212P.  
XX PR 17-OCT-1997; 97US-0062250P. 05-JUN-1998; 98US-0088217P.  
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XX PR 13-NOV-1997; 97US-00653120P. 11-JUN-1998; 98US-0088861P.  
XX PR 24-NOV-1997; 97US-006561120P. 11-JUN-1998; 98US-0088861P.  
XX PR 24-NOV-1997; 97US-00656466P. 11-JUN-1998; 98US-0088861P.  
XX PR 11-DEC-1997; 97US-0069335P. 11-JUN-1998; 98US-0088861P.  
XX PR 17-DEC-1997; 97US-0069425P. 11-JUN-1998; 98US-0088861P.  
XX PR 17-DEC-1997; 97US-0069870P. 11-JUN-1998; 98US-0088861P.  
XX PR 18-DEC-1997; 97US-0068017P. 11-JUN-1998; 98US-0088861P.  
XX PR 10-MAR-1998; 98US-0077450P. 11-JUN-1998; 98US-0088861P.  
XX PR 11-MAR-1998; 98US-0077632P. 11-JUN-1998; 98US-0088861P.  
XX PR 11-MAR-1998; 98US-0077643P. 11-JUN-1998; 98US-0088861P.  
XX PR 20-MAR-1998; 98US-0078856P. 11-JUN-1998; 98US-0088861P.  
XX PR 20-MAR-1998; 98US-0078939P. 11-JUN-1998; 98US-0088861P.  
XX PR 27-MAR-1998; 98US-0079664P. 11-JUN-1998; 98US-0088861P.  
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XX PR 31-MAR-1998; 98US-0080107P. 11-JUN-1998; 98US-0088861P.  
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XX PR 15-APR-1998; 98US-0081838P. 11-JUN-1998; 98US-0088861P.  
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XX PR 29-APR-1998; 98US-0083559P. 11-JUN-1998; 98US-0088861P.  
XX PR 05-MAY-1998; 98US-0084366P. 11-JUN-1998; 98US-0088861P.  
XX PR 06-MAY-1998; 98US-0084414P. 11-JUN-1998; 98US-0088861P.  
XX PR 07-MAY-1998; 98US-0084639P. 11-JUN-1998; 98US-0088861P.  
XX PR 07-MAY-1998; 98US-0084640P. 11-JUN-1998; 98US-0088861P.  
XX PR 07-MAY-1998; 98US-0084643P. 11-JUN-1998; 98US-0088861P.  
XX PR 15-MAY-1998; 98US-0085579P. 11-JUN-1998; 98US-0088861P.  
XX PR 15-MAY-1998; 98US-0085580P. 11-JUN-1998; 98US-0088861P.  
XX PR 15-MAY-1998; 98US-0085582P. 11-JUN-1998; 98US-0088861P.  
XX PR 15-MAY-1998; 98US-0085700P. 11-JUN-1998; 98US-0088861P.

PR	18-AUG-1998;	98US-0096949P.	Query Match	65.1%;	Score 2026.5;	DB 6;	Length 545;
PR	18-AUG-1998;	98US-0096959P.	Best Local Similarity	80.3%;	Pred. No. 2.8e-183;		
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PR	26-AUG-1998;	98US-0097954P.					
PR	26-AUG-1998;	98US-0097955P.					
PR	26-AUG-1998;	98US-0097971P.					
PR	26-AUG-1998;	98US-0097974P.					
PR	26-AUG-1998;	98US-0098014P.					
PR	01-SEP-1998;	98US-0098716P.					
PR	01-SEP-1998;	98US-0098723P.					
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PR	10-SEP-1998;	98US-0099754P.					
PR	10-SEP-1998;	98US-0099763P.					
PR	10-SEP-1998;	98US-0099812P.					
PR	15-SEP-1998;	98US-0100388P.					
PR	16-SEP-1998;	98US-0100662P.					
PR	16-SEP-1998;	98US-0100664P.					
PR	16-SEP-1998;	98US-0101751P.					
PR	16-SEP-1998;	98US-0101751P.					
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PR	17-SEP-1998;	98US-0100684P.					
PR	17-SEP-1998;	98US-0100915P.					
PR	17-SEP-1998;	98US-0100930P.					
PR	18-SEP-1998;	98US-0100849P.					
PR	18-SEP-1998;	98US-0101014P.					
PR	18-SEP-1998;	98US-0101068P.					
PR	23-SEP-1998;	98US-0101471P.					
PR	23-SEP-1998;	98US-0101472P.					
PR	23-SEP-1998;	98US-0101475P.					
PR	23-SEP-1998;	98US-0101477P.					
PR	24-SEP-1998;	98US-0101738P.					
PR	24-SEP-1998;	98US-0101739P.					
PR	24-SEP-1998;	98US-0101743P.					
PR	24-SEP-1998;	98US-0101922P.					
PR	25-SEP-1998;	98US-0101786P.					
PR	29-SEP-1998;	98US-0102207P.					
PR	29-SEP-1998;	98US-0102240P.					
PR	29-SEP-1998;	98US-0102330P.					
PR	29-SEP-1998;	98US-0102331P.					
PR	30-SEP-1998;	98US-0102487P.					
PR	30-SEP-1998;	98US-0102570P.					
PR	30-SEP-1998;	98US-0102571P.					
PR	01-OCT-1998;	98US-0102684P.					
PR	01-OCT-1998;	98US-0102687P.					
PR	02-OCT-1998;	98US-0102965P.					
PR	06-OCT-1998;	98US-0103258P.					
PR	06-OCT-1998;	98US-0103449P.					
PR	07-OCT-1998;	98US-00168978.					

Query Match 65.1%; Score 2026.5; DB 6; Length 545;

Best Local Similarity 80.3%; Pred. No. 2.8e-183;

Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

QY	6	LPSTVLPSSLTPAGAGMSRWILCWSLTLCLMAOTALCALHTKRPQVVKYGLQGMH	65
DB	47	LGSTSTPATTAPSSGGFTGLFGSKPATGFTLGGTNGTALHTKRPQVVKYGLQGMH	106
QY	66	VGKTPIQVFLGVFFSRPPLGLIRFAPPEPFPWKGRDATTYPG	110
DB	107	VGKTPIQVFLGVFFSRPPLGLIRFAPPEPFPWKGRDATTYPGWSIALSPGWSAVARS	166
QY	111	-----CLOESGOLASMYSTRERYKMLRFSEDCILYLVY	145
DB	167	RLTATSASRVQASLLPQLFSVNGVYECLOESGQLASMTVSTRERYKMLRFSEDCILYLVY	226
QY	146	APARAPGPQPLPMVWFFGGAFIVGAASSYEGSDLAAREKVVLPQLHRLGIFGFLSTDD	205
DB	227	APARAPGPQPLPMVWFFGGAFIVGAASSYEGSDLAAREKVVLPQLHRLGIFGFLSTDD	286

QY	206	SHARGNWLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMWSPLASGLFHR	265
DB	287	SHARGNWLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMWSPLASGLFHR	346
QY	266	AISQSGTALFRLFTITSNPLKVAKKVAHLACNHNSTQILVNCRLALSGLTKVMRYSNRQRF	325
DB	347	AISQSGTALFRLFTITSNPLKVAKKVAHLACNHNSTQILVNCRLALSGLTKVMRYSNRQRF	406
QY	326	LQNFQRPDPPEIIWMSFVVDGVVIPPDPVLLLTQGVKSSVPYLLGVNNLEFNWLLPYIM	385
DB	407	LQNFQRPDPPEIIWMSFVVDGVVIPPDPVLLLTQGVKSSVPYLLGVNNLEFNWLLPY--	464
QY	386	KFPLNRQAMRKETITKMLWSTRLNITKQVPLVVEEYLDNVNNEHDKWKLRRNMDIVQ	445
DB	465	-----NITKEQVPLVVEEYLDNVNNEHDKWKLRRNMDIVQ	499
QY	446	DATFYATLQTAHYRD	462
DB	500	DATFYATLQTAHYRE	516
RESULT 9			
ABR66165			
ID	ABR66165 standard; protein; 545 AA.		
XX	AC ABR66165;		
XX	XX		
DT	05-AUG-2003 (first entry)		
DE	Human secreted polypeptide PRO873, SEQ ID NO:58.		
KW	Human; PRO; secreted protein; transmembrane protein;		
KW	extracellular domain; tumour necrosis factor-alpha; TNF-alpha;		
KW	chondrocyte; proliferation; differentiation; cartilage disorder;		
KW	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;		
KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;		
KW	liver; drug screening; transgenic animal; genetic analysis;		
KW	antiarthritic; vulnery; Gene therapy.		
OS	Homo sapiens.		
XX	US2003027278-A1.		
XX	06-FEB-2003.		
XX	21-JUN-2002; 2002US-00176987.		
XX	18-SEP-1997; 97US-0059263P.		
PR	18-SEP-1997; 97US-0059266P.		
PR	17-OCT-1997; 97US-0062250P.		
PR	21-OCT-1997; 97US-0063486P.		
PR	24-OCT-1997; 97US-0063120P.		
PR	24-OCT-1997; 97US-0063121P.		
PR	28-OCT-1997; 97US-0063540P.		
PR	28-OCT-1997; 97US-0063541P.		
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PR	28-OCT-1997; 97US-0063564P.		
PR	29-OCT-1997; 97US-0063734P.		
PR	31-OCT-1997; 97US-0063870P.		
PR	31-OCT-1997; 97US-0064103P.		
PR	13-NOV-1997; 97US-0065311P.		
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PR	24-NOV-1997; 97US-0066772P.		
PR	11-DEC-1997; 97US-0069335P.		
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PR	17-DEC-1997; 97US-0069870P.		
PR	18-DEC-1997; 97US-0068017P.		
PR	10-MAR-1998; 98US-0077450P.		
PR	11-MAR-1998; 98US-0077632P.		
PR	11-MAR-1998; 98US-0077649P.		
PR	20-MAR-1998; 98US-0078866P.		

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PR 24-SEP-1998; 98US-0101922P.  
PR 25-SEP-1998; 98US-0101786P.  
PR 29-SEP-1998; 98US-0102207P.  
PR 29-SEP-1998; 98US-0102240P.  
PR 29-SEP-1998; 98US-0102330P.  
PR 29-SEP-1998; 98US-0102331P.

PR	30-SEP-1998;	98US-0102487P.	
PR	30-SEP-1998;	98US-0102570P.	
PR	30-SEP-1998;	98US-0102571P.	
PR	01-OCT-1998;	98US-0102684P.	
PR	01-OCT-1998;	98US-0102687P.	
Query Match			
Best Local Similarity 65.1%; Score 2026.5; DB 6; Length 545;			
Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;			
QY	6	LPSTVPLSLPTAGAGMSRWILCWSLTLCLMAQALGALHTKRPQVVTKYGTLOGKQWH	65
DB	47	LGSTSTPATTSAPSSGFTGLFGSKPATGFTLGGTNTGALHTKRPQVVTKYGTLOGKQWH	106
QY	66	VGKTPIQVFLGVFSPRPPIILRPAPPEPPEPWKGRDATTTPPG-----	110
DB	107	VGKTPIQVFLGVFSPRPPIILRPAPPEPPEPWKGRDATTTPPGWSLSPCWSAVARS	166
QY	111	-----CLOESWGOLASMYSTRERYKWLRFSDCLYLVNY	145
DB	167	RLTATSASRVOASLLPQPLSVWGYRCLQESWGOLASMYSTRERYKWLRFSDCLYLVNY	226
QY	146	APARAPGDPQLPVMWFFPGGAFIVGAASSYEGSDLAAREKVVLFVLOHRLGIFGFLSTDD	205
DB	227	APARAPGDPQLPVMWFFPGGAFIVGAASSYEGSDLAAREKVVLFVLOHRLGIFGFLSTDD	286
QY	206	SHARGNWLLDDQAALRWQENIAAEGDGNVTLFGQSAGAMSIISGLMWSPLASGLFHR	265
DB	287	SHARGNWLLDDQAALRWQENIAAEGDGNVTLFGQSAGAMSIISGLMWSPLASGLFHR	346
QY	266	AISQSGTALFRLFTTSNPLKVAKKVAHLACGNHNSITQILVNCILRALSGTKVMKRVSNKMF	325
DB	347	AISQSGTALFRLFTTSNPLKVAKKVAHLACGNHNSITQILVNCILRALSGTKVMKRVSNKMF	406
QY	326	LQNFORDPBEIWSMSPVGVVIPPDDPLVLTQGVKSSVPYLLGVNNLEFNWLLPYIM	385
DB	407	LQNFORDPBEIWSMSPVGVVIPPDDPLVLTQGVKSSVPYLLGVNNLEFNWLLPY--	464
QY	386	KFPLNRQMRKETITKMLSTRLLNITKQVPLVVEEYLDNVEDWKLNRNMDIVQ	445
DB	465	-----NITKQVPLVVEEYLDNVEDWKLNRNMDIVQ	459
QY	446	DATEVYATLQTAHYHRD	462
DB	500	DATEVYATLQTAHYHRE	516
RESULT 10			
ID	ABR65555	standard; protein; 545 AA.	
XX	AC	ABR65555;	
XX	DE	(first entry)	
XX	DE	Human secreted polypeptide PRO873, SEQ ID NO:58.	
XX	KW	Human; PRO; secreted protein; transmembrane protein;	
XX	KW	extracellular domain; tumour necrosis factor-alpha; TNF-alpha;	
XX	KW	chondrocyte; proliferation; differentiation; cartilage disorder;	
XX	KW	bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;	
XX	KW	adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;	
XX	KW	liver; drug screening; transgenic animal; genetic analysis;	
XX	KW	antiarthritic; vulnery; gene therapy.	
XX	OS	Homo sapiens.	
XX	PN	US2003036159-A1.	
XX	PD	20-FEB-2003.	
XX	PF	02-JUL-2002; 2002US-00188773.	

PR	18-SEP-1997;	98US-0059263P.	
PR	18-SEP-1997;	98US-0059266P.	
PR	17-OCT-1997;	98US-0062250P.	
PR	21-OCT-1997;	98US-0063486P.	
PR	24-OCT-1997;	98US-0063120P.	
PR	24-OCT-1997;	98US-0063121P.	
PR	28-OCT-1997;	98US-0063540P.	
PR	28-OCT-1997;	98US-0063541P.	
PR	28-OCT-1997;	98US-0063544P.	
PR	28-OCT-1997;	98US-0063564P.	
PR	29-OCT-1997;	98US-0063734P.	
PR	31-OCT-1997;	98US-0063870P.	
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PR	13-NOV-1997;	98US-0065311P.	
PR	21-NOV-1997;	98US-0065120P.	
PR	24-NOV-1997;	98US-0065466P.	
PR	24-NOV-1997;	98US-0066772P.	
PR	12-DEC-1997;	98US-0069335P.	
PR	17-DEC-1997;	98US-0069870P.	
PR	18-DEC-1997;	98US-0068017P.	
PR	10-MAR-1998;	98US-0077450P.	
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PR	27-MAR-1998;	98US-0080107P.	
PR	31-MAR-1998;	98US-0080194P.	
PR	01-APR-1998;	98US-0080327P.	
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PR	09-APR-1998;	98US-0081195P.	
PR	15-APR-1998;	98US-0081838P.	
PR	21-APR-1998;	98US-0082568P.	
PR	21-APR-1998;	98US-0082569P.	
PR	22-APR-1998;	98US-0082704P.	
PR	22-APR-1998;	98US-0082797P.	
PR	28-APR-1998;	98US-0083322P.	
PR	29-APR-1998;	98US-0083495P.	
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PR	05-MAY-1998;	98US-0084366P.	
PR	06-MAY-1998;	98US-0084414P.	
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PR	18-AUG-1998;	98US-0096959P.
PR	18-AUG-1998;	98US-0097022P.
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Query Match 65.1%; Score 2026.5; DB 6; Length 545;

Best Local Similarity 80.3%; Pred. No. 2.8e-183;  
Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

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DB	47	LGSTSTATTSSAPSSGFGTGLFGSKPATGFTLGTTNGALHTKRPQVWTKYGTLOGKQH 106
QY	66	VKTPIQVFLGVFPSPRLPGLILFAPPEPPKWKIRDAATYPGWSLSPGWSAVARS 166
DB	107	VKTPIQVFLGVFPSPRLPGLILFAPPEPPKWKIRDAATYPGWSLSPGWSAVARS 166
QY	111	-----CLQESWGOLASMYVSTRERYKWLRFSEDCILYNY 110
DB	167	RLTATSASRVQASLLPQLPSVWGYRCLQESWGOLASMYVSTRERYKWLRFSEDCILYNY 226
QY	146	APAPAGDPOLPVNVPFGGAFIVGAASSYEGSDLAAREKVLVFLQHLGIFGFLSTDD 205
DB	227	APAPAGDPOLPVNVPFGGAFIVGAASSYEGSDLAAREKVLVFLQHLGIFGFLSTDD 286
QY	206	SHARGNGLLDQVAALRWQENIAAEGDPNVTLFGQSAGANSISGLMSPGLASGLFHR 265
DB	287	SHARGNGLLDQVAALRWQENIAAEGDPNVTLFGQSAGANSISGLMSPGLASGLFHR 346
QY	266	AISQSGTALFRLFITSNPLKVAKVAFLACGNHNSTQILVNCRLALSGLTKWVSVNMRP 325
DB	347	AISQSGTALFRLFITSNPLKVAKVAFLACGNHNSTQILVNCRLALSGLTKWVSVNMRP 406
QY	326	LQNFQDPEEIIWMSPPVGVVIPPDDPLVLTQKYSVPYLLGVNNLEFNLLPYM 385
DB	407	LQNFQDPEEIIWMSPPVGVVIPPDDPLVLTQKYSVPYLLGVNNLEFNLLPYM 464
QY	386	KFPLNQMRKETITKMLMSTRLLNITKEQVPLVVEEYLDNVDNHDWMLNRMMDIVQ 445
DB	465	-----NITKEQVPLVVEEYLDNVDNHDWMLNRMMDIVQ 499
QY	446	DATFVYATLQTAHYHRD 462
DB	500	DATFVYATLQTAHYHRE 516

RESULT 11

ABU99495  
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XX AC ABU99495;  
XX 09-AUG-2003 (first entry)  
DT Human secreted/transmembrane protein (PRO) #29.  
XX Human; secreted and transmembrane protein; PRO; TNF-alpha;  
KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
KW tissue typing.  
XX Homo sapiens.  
OS  
XX US2003040070-A1.  
PN  
XX 27-FEB-2003.  
PD  
XX 27-JUN-2002; 2002US-00184627.  
PF  
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PR	29-SEP-1998;	98US-0102207P.	
PR	29-SEP-1998;	98US-0102240P.	
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PR	29-SEP-1998;	98US-0102331P.	
PR	30-SEP-1998;	98US-0102487P.	
PR	30-SEP-1998;	98US-0102570P.	
PR	01-OCT-1998;	98US-0102571P.	
PR	01-OCT-1998;	98US-0102687P.	
PR	02-OCT-1998;	98US-0102965P.	
PR	06-OCT-1998;	98US-0103258P.	
PR	06-OCT-1998;	98US-0103449P.	
PR	07-OCT-1998;	98US-0106997P.	
Query Match	65.1%;	Score 2026.5;	DB 6; Length 545;
Best Local Similarity	80.3%;	Pred. No. 2.8e-183;	
Matches 399;	Conservative	5; Mismatches 26;	Indels 67; Gaps 2;
QY	6	LPSTVPLSLPTAGAGSWILCNLTCLMAQTALGALHTKRPQVTKYTLQKQKH 65	
Db	47	LGSTSTPATTSSAFSGFTGLFGSKPATGFTTGGTNGALTKRPQVTKYTLQKQKH 106	
QY	66	VGKTIQVFLGVFPSPPLILRFAPPEPEPKGIRDTATTPPG-----110	
Db	107	VGKTIQVFLGVFPSPPLILRFAPPEPEPKGIRDTATTPPGWSLSPGSAVARS 166	
QY	111	-----CLOESWGLASMYSTRERYKWLRFSEDCILYLVNY 145	
Db	167	RLTATSASRVQASLLPQLSVNGYRCLOESWGLASMYSTRERYKWLRFSEDCILYLVNY 226	
QY	146	APARAPGDPOLPVMVWFFGAFIVCAASSYEGSDLAAREKVVLFQHRLGIFGFLSTDD 205	

Db	227	APARAPGDPOLPVMVWFFGAFIVCAASSYEGSDLAAREKVVLFQHRLGIFGFLSTDD 286	
QY	206	SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMSPGLASGLFHR 265	
Db	287	SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTLFGQSAGAMSISGLMSPGLASGLFHR 346	
QY	266	AISQSGTALFRLFITSNPLKVAKKVAHLAGCNHSTQILVNCRLALSGTKVMRYSNQKRF 325	
Db	347	AISQSGTALFRLFITSNPLKVAKKVAHLAGCNHSTQILVNCRLALSGTKVMRYSNQKRF 406	
QY	326	LQNFQRPDEIIMSPPVGVIPDDPLVLLTQGVSSVPYLLGVNNLEFNWLLPYIM 385	
Db	407	LQNFQRPDEIIMSPPVGVIPDDPLVLLTQGVSSVPYLLGVNNLEFNWLLPY-- 464	
QY	386	KEPLNRQAVRKETITKMLKSTRTLLNITKEOVPLVVEEYLDNNEHDKMLRNMMDIVQ 445	
Db	465	-----NITKEOVPLVVEEYLDNNEHDKMLRNMMDIVQ 499	
QY	446	DATFYATLQTAHYRD 462	
Db	500	DATFYATLQTAHYRE 516	
RESULT 12			
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ID	ABU82734	standard; protein; 545 AA.	
XX	AC	ABU82734;	
XX	DT	27-JUN-2003 (first entry)	
XX	DE	Human PRO polypeptide #29.	
XX	KW	Human; PRO polypeptide; secreted and transmembrane protein; tumour;	
XX	OS	chromosome mapping; gene mapping; cytostatic.	
XX	PN	Homo sapiens.	
XX	PD	US2003032113-A1.	
XX	PF	13-FEB-2003.	
XX	PR	20-JUN-2002; 2002US-00176911.	
XX	PR	18-SEP-1997; 97US-0059263P.	
XX	PR	18-SEP-1997; 97US-0059266P.	
XX	PR	17-OCT-1997; 97US-0062250P.	
XX	PR	21-OCT-1997; 97US-0063486P.	
XX	PR	24-OCT-1997; 97US-0063120P.	
XX	PR	24-OCT-1997; 97US-0063121P.	
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XX	PR	28-OCT-1997; 97US-0063564P.	
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XX	PR	13-NOV-1997; 97US-0065311P.	
XX	PR	21-NOV-1997; 97US-0066120P.	
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PR	02-JUL-1998	98US-0091626P
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PR	02-JUL-1998	98US-0091632P
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PR	09-SEP-1998	98US-0099602P
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PR	10-SEP-1998	98US-0099763P
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RESULT 14  
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XX  
AC ABR68104;  
DT 11-AUG-2003 (first entry)  
XX  
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KW Human; PRO; secreted protein; transmembrane protein;  
KW extracellular domain; tumour necrosis factor-alpha; TNF-alpha;  
KW chondrocyte; proliferation; differentiation; cartilage disorder;  
KW bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
KW adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
KW liver; drug screening; transgenic animal; genetic analysis;  
KW antiarthritic; vulnary; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN US2003027264-A1.  
PD 06-FEB-2003.  
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XX 18-JUN-2002; 2002US-00174579.  
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PR	10-AUG-1998;	98US-0096012P.	146		
PR	17-AUG-1998;	98US-0096757P.	227	APARAPGDPOLPYVMWPPGAFIVGAASSYEGSDLAAREKVLVFLQHRIGIFGLSTDD	286
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PR	18-AUG-1998;	98US-0097022P.	266		
PR	26-AUG-1998;	98US-0097952P.	347	AISOSGTALFRLFTTSNPLKVAHVLAHAGNHNSTOILVNCRLALSGTKVMRVSNKQRF	406
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PR	26-AUG-1998;	98US-0097971P.	326		
PR	26-AUG-1998;	98US-0097977P.	407	LQLNFQRPDEPIIWSMSFVVDGVIPDDPLVLLTQGVKSVVPYLLGVNNLEFNWLLPY--	464
PR	26-AUG-1998;	98US-0097974P.	407		
PR	26-AUG-1998;	98US-0098014P.	386	KFPLNRQMRKXETITKMLWSTRTLLNITKSOVPLVVEEYLDNVNEHDKVLRNEMDIVQ	445
PR	01-SEP-1998;	98US-0098716P.	386		
PR	01-SEP-1998;	98US-0098723P.	465	-----NITKEQVPLVVEEYLDNVNEHDKVLRNEMDIVQ	499
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PR	09-SEP-1998;	98US-0099602P.	446	DATFYATLQTAHYHRD	462
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PR	10-SEP-1998;	98US-0099754P.	500	DATFYATLQTAHYHRE	516
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DB	47	LGSTSTPATTAPSGFGTGFSGKPGATGFTLGGTNTGALHTKRPQVVTYKGTLOGKQMH	106		
QY	66	VGKTIQVFLGVFRRPLGILRAPPEPPFWKGIKRDATTPPG-----	110		
DB	107	VGKTIQVFLGVFRRPLGILRAPPEPPFWKGIKRDATTPPGWSLALSPGWSAVARS	166		
QY	111	-----CLOESWGOLASVMVSTRERYKMLRFSDCCLYLVNY	145		
DB	167	RLTATSASRVOASLLPQLPSVNGVRCLOESWGOLASVMVSTRERYKMLRFSDCCLYLVNY	226		

RESULT 15  
ABU96157  
ID ABU96157 standard; protein; 545 AA.  
XX AC ABU96157;  
XX AC ABU96157;  
XX DT 25-JUL-2003 (first entry)  
XX DE Novel human secreted and transmembrane protein PRO873.  
XX KW Human; secreted and transmembrane protein; PRO; transgenic animal;  
KW knockout; chromosome identification; tissue typing; tumour;  
KW chondrocyte proliferation; chondrocyte differentiation;  
KW tumor necrosis factor-alpha release stimulator.  
XX OS Homo sapiens.  
XX US2003036144-A1.  
XX PD 20-FEB-2003.  
XX PF 01-JUL-2002; 2002US-00187601.  
XX PR 18-SEP-1997; 97US-0059263P.  
PR 18-SEP-1997; 97US-0059266P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 21-OCT-1997; 97US-0063486P.  
PR 24-OCT-1997; 97US-0063120P.  
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PR 28-OCT-1997; 97US-0063541P.  
PR 28-OCT-1997; 97US-0063544P.  
PR 28-OCT-1997; 97US-0063564P.  
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PR 13-NOV-1997; 97US-0065311P.  
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PR 20-MAR-1998; 98US-0078886P.  
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	1169.5	37.6	584	3	US-09-150-515-2
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8	983.5	31.6	454	3	US-08-446-100-26
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14	909.5	29.2	574	4	US-10-023-515-4
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23	787	25.3	600	3	US-08-975-084-1
24	787	25.3	614	1	US-07-732-962A-2
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32	783	25.2	614	3	US-08-446-100-23	Sequence 23, Appl
33	782	25.1	614	3	US-08-446-100-22	Sequence 22, Appl
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ALIGNMENTS

RESULT 1  
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; Sequence 2, Application US/09264737A  
; Patent No. 6107549  
; GENERAL INFORMATION:  
; APPLICANT: Ruff, Paul C.C.  
; TITLE OF INVENTION: Engineering Plant Resistance to Pyridines via  
; TITLE OF INVENTION: Expression of Esterase Enzymes  
; FILE REFERENCE: 38-21(10551) RLE3 Pyridine Tolerance  
; CURRENT APPLICATION NUMBER: US/09/264,737A  
; EARLIER FILING DATE: 1999-03-09  
; EARLIER APPLICATION NUMBER: 60/077,377  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 566  
; TYPE: PRT  
; ORGANISM: Rabbit  
US-09-264-737-2

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RESULT 2  
 US-08-845-295A-2  
 ; Sequence 2, Application US/08845295A  
 ; Patent No. 5817490  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hubbs, John C.  
 ; TITLE OF INVENTION: Enzymatic Process for the Manufacture of  
 ; TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of  
 ; TITLE OF INVENTION: 2-Keto-L-Gulonic Acid  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Eastman Chemical Company  
 ; STREET: P.O. Box 511  
 ; CITY: Kingsport  
 ; STATE: Tennessee  
 ; COUNTRY: USA  
 ; ZIP: 37662-5075  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch disk  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows 95  
 ; SOFTWARE: Microsoft Word  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/845,295A  
 ; FILING DATE: 25-April-97  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/017,879  
 ; FILING DATE: 17-MAY-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Cheryl J. Tubach  
 ; REGISTRATION NUMBER: 38,346  
 ; REFERENCE/DOCKET NUMBER: 70432  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 423-229-6189  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 584 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear  
 ; MOLECULE TYPE: protein  
 ; US-08-845-295A-2

Query Match 37.6%; Score 1169.5; DB 2; Length 584;  
 Best Local Similarity 43.0%; Pred. No. 6.9e-111;  
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 DB 537 YDQEGYLQIGVNTQAAKRLKGEVAFWNDLLSKEAAKK 575

RESULT 3  
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 ; Sequence 2, Application US/09140933  
 ; Patent No. 602719  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hubbs, John C.  
 ; TITLE OF INVENTION: Enzymatic Process for the Manufacture of  
 ; TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of  
 ; TITLE OF INVENTION: 2-Keto-L-Gulonic Acid  
 ; NUMBER OF SEQUENCES: 3  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Eastman Chemical Company  
 ; STREET: P.O. Box 511  
 ; CITY: Kingsport  
 ; STATE: Tennessee  
 ; COUNTRY: USA  
 ; ZIP: 37662-5075  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch disk  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows 95  
 ; SOFTWARE: Microsoft Word  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/140,933  
 ; FILING DATE: 27-August-98  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/017,879; 08/845,295  
 ; FILING DATE: 17-May-96; 25-April-97  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Cheryl J. Tubach  
 ; REGISTRATION NUMBER: 38,346  
 ; REFERENCE/DOCKET NUMBER: 70432  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 423-229-6189  
 ; TELEFAX: 423-229-1239  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 584 amino acids  
 ; TYPE: Amino Acid

```

; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-09-140-933-2

Query Match      37.6%; Score 1169.5; DB 3; Length 584;
Best Local Similarity 43.0%; Pred. No. 6.9e-111;
Matches 249; Conservative 108; Mismatches 193; Indels 29; Gaps 13;

QY 26 WILCWSLTLCLMAQTALGALHTKRPQV-TKYGTLOGKQMHVG-----KTIQVFLGVPEFS 80
DB 2 WLL--PLVLTSLASSATWAGQSPVVDTAQGRVLGKYVSLGLEAFTQPVAVFLGVPEFA 59

QY 81 RPLGLILREAPPPEPPKIRDTATYPGCLQESWGQLASMYST----KTIQVFLGVPEFS 80
DB 60 KPPLGSLURFAPPQAPPEPWSFKNTISYPPMCCQDPVVEQMTSLDFTNFTGKERLT-LBFS 118

QY 137 EDCLYLNVYAPAPGDPQLPMVWFPFGAFIVGAASSYEGSDLAAREK--VVLVFLQHR 194
DB 119 EDCLYLNIYTPADLTGRGLPVMVWIHGGGLVGGAPYDGVVLAHAHENFTVVVAIQYR 178

QY 195 LGIFGFLSTDDSHARGNWLDDQALRWQENIAAFGGDPGNVTLFGQS--AGAMSISG 252
DB 179 LGIWGFFSTGDEHSRGNWGHLDQVAALHWQENIANFNGDPSGVTIFGESFTAGGESVS 238

QY 253 LKMSPLASGLFHRAISQSGTALFRLFTISNPLKVAKKVAHLACGNHNSIQI--LVNCLRA 310
DB 239 LVLSPLAKNLFHRAISQSGVALTVLVRKDKMAAKQIAVLGCKTTSVAVFTFVHCLRQ 298

QY 311 LSGTKVMRVSNKRFLOINQFQDPPEIILWMSFPVVDGVVTPDDPLVLLTQG--KVSSVVPY 368
DB 299 KSEDELLDLTLKMKFLTLDFHGDQRESHFPLTPVVDGVLPPKPEEILAEKDFTFNTV 358

QY 369 LLGVNNLEFNWLLPYIMKFLNRQAMRKETITKMLWSTRTLLNITKEQVPLV--VEEYLD 426
DB 359 IVGINKQEFGLLPTMNGEPLSEGKLDOKTATSLWKSYPANIPEELTPVATFTDKYL 418

QY 427 NVNEHDKMLRNRMMDIVQDATFYATLOTAYHRDAGLPVLYEPEHH---ARGIIVKP 483
DB 419 GTDDPVKK--KDLFLDLMGDVVFGVPSVTVARQHRDAGAPTYMYEFQYRPSFSSDKFTK 476

QY 484 RTDGADHGDENYFLFGGPFATGLSMGKEKALSLOMKYKWFANFARTGNPDGNLPCWP--R 541
DB 477 KTVIGDHGDEIFSVFGFLLKGDAPEEVLSKTVMKFWANFARSNPNGEGLPHPFTM 536

QY 542 YNKDEKYLQDLFTTRVGMKLEKKMAFWMSLYQSQRPEK 580
DB 537 YDQEGYLIQVNTQAARKLKGEEVAFWNDDLKSEAAKK 575

RESULT 4
US-09-146-661-2
; Sequence 2, Application US/09146661
; Patent No. 6136575
; GENERAL INFORMATION:
; APPLICANT: Hubbs, John C.
; TITLE OF INVENTION: Enzymatic Process for the Manufacture of
; TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eastman Chemical Company
; STREET: P.O. Box 511
; STATE: Tennessee
; COUNTRY: USA
; ZIP: 37662-5075
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch disk
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/146,661

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; FILING DATE: 03-September-98
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER: US 60/017,879; 08/845,295
; FILING DATE: 17-May-96; 25-April-97
; ATTORNEY/AGENT INFORMATION:
; NAME: Cheryl J. Tubach
; REGISTRATION NUMBER: 38,346
; REFERENCE/DOCKET NUMBER: 70432
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 423-229-6189
; TELEFAX: 423-229-1239
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 584 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
US-09-146-661-2

Query Match      37.6%; Score 1169.5; DB 3; Length 584;
Best Local Similarity 43.0%; Pred. No. 6.9e-111;
Matches 249; Conservative 108; Mismatches 193; Indels 29; Gaps 13;

QY 26 WILCWSLTLCLMAQTALGALHTKRPQV-TKYGTLOGKQMHVG-----KTIQVFLGVPEFS 80
DB 2 WLL--PLVLTSLASSATWAGQSPVVDTAQGRVLGKYVSLGLEAFTQPVAVFLGVPEFA 59

QY 81 RPLGLILREAPPPEPPKIRDTATYPGCLQESWGQLASMYST----KTIQVFLGVPEFS 136
DB 60 KPPLGSLURFAPPQAPPEPWSFKNTISYPPMCCQDPVVEQMTSLDFTNFTGKERLT-LBFS 118

QY 137 EDCLYLNVYAPAPGDPQLPMVWFPFGAFIVGAASSYEGSDLAAREK--VVLVFLQHR 194
DB 119 EDCLYLNIYTPADLTGRGLPVMVWIHGGGLVGGAPYDGVVLAHAHENFTVVVAIQYR 178

QY 195 LGIFGFLSTDDSHARGNWLDDQALRWQENIAAFGGDPGNVTLFGQS--AGAMSISG 252
DB 179 LGIWGFFSTGDEHSRGNWGHLDQVAALHWQENIANFNGDPSGVTIFGESFTAGGESVS 238

QY 253 LKMSPLASGLFHRAISQSGTALFRLFTISNPLKVAKKVAHLACGNHNSIQI--LVNCLRA 310
DB 239 LVLSPLAKNLFHRAISQSGVALTVLVRKDKMAAKQIAVLGCKTTSVAVFTFVHCLRQ 298

QY 311 LSGTKVMRVSNKRFLOINQFQDPPEIILWMSFPVVDGVVTPDDPLVLLTQG--KVSSVVPY 368
DB 299 KSEDELLDLTLKMKFLTLDFHGDQRESHFPLTPVVDGVLPPKPEEILAEKDFTFNTV 358

QY 369 LLGVNNLEFNWLLPYIMKFLNRQAMRKETITKMLWSTRTLLNITKEQVPLV--VEEYLD 426
DB 359 IVGINKQEFGLLPTMNGEPLSEGKLDOKTATSLWKSYPANIPEELTPVATFTDKYL 418

QY 427 NVNEHDKMLRNRMMDIVQDATFYATLOTAYHRDAGLPVLYEPEHH---ARGIIVKP 483
DB 419 GTDDPVKK--KDLFLDLMGDVVFGVPSVTVARQHRDAGAPTYMYEFQYRPSFSSDKFTK 476

QY 484 RTDGADHGDENYFLFGGPFATGLSMGKEKALSLOMKYKWFANFARTGNPDGNLPCWP--R 541
DB 477 KTVIGDHGDEIFSVFGFLLKGDAPEEVLSKTVMKFWANFARSNPNGEGLPHPFTM 536

QY 542 YNKDEKYLQDLFTTRVGMKLEKKMAFWMSLYQSQRPEK 580
DB 537 YDQEGYLIQVNTQAARKLKGEEVAFWNDDLKSEAAKK 575

RESULT 5
US-09-150-515-2
; Sequence 2, Application US/09150515
; Patent No. 6271006
; GENERAL INFORMATION:
; APPLICANT: Hubbs, John C.
; TITLE OF INVENTION: Enzymatic Process for the Manufacture of
; TITLE OF INVENTION: Ascorbic Acid, 2-Keto-L-Gulonic Acid, and Esters of

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Db 1 EHCLYLNIVTPADLTKKNLPPVMVWIIHGGGLMVGAASYDGLAALAHENVVVVTIQYRLG 60
QY 197 IFGFLSTDDSHARGNWGLLDQVAALRWQENIAAFGGDPGNVTLFGOSAGASISGLMMS 256
Db 61 IWGFFSTGDEHSRGNWGHLDQVAALRWQDNIAFSGNPGSVTIIFGSGAGSVSVLVLS 120
QY 257 PLASGLFHRAISQSGTALFRLFITSNPLK-VAKKVAHLACNHNSTQILVNCRLALSGTK 315
Db 121 FLAKNLFHRAISGVALTSVLVKGDKVPLAEQIAITAGCKTTTSAAMVHCLAQKTEEE 180
QY 316 VMRSVNMRFLOLNFORDPEEIIWMSFVVDGVVVDVLLVLTQGVSSVYLLGVNVL 375
Db 181 LLETTLKIGNSYLWYRETQRESHLLGTVIDGMLLKTPEELQRENFHTVPMVGINKQ 240
QY 376 EFNWLLP-YIMKFLPNRQAMEKETTITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWK 434
Db 241 EFGWLLPQMLMSYPLSEGQDQKTAMSLGSPFLFAIAKELIPEATEKYLGGTD--DTV 298
QY 435 MLNRNMDIVODATFVYATLQTAHYHRDAGLPVLYIEFEHH-ARGIIVKPRDGDAGHDE 493
Db 299 KKKDLILDIAVDMFVPSVIVARNHRDAGAPTYMYEFQYRPFSSDMKPKTVIGDHGDE 358
QY 494 MYFLFGGPFATGLSMGKEKALSQMKMYANFARTGNPDGNLPCWPRYNKDEKYLQDF 553
Db 359 LFSVFGAPFLKEGASEEIEIRLSKVMKFWANFARNGNPKGLPHWPEYNQKEGYLQIGA 418
QY 554 TTRVGMKLEKKMAFMWSLYQSQRPEKORQ 583
Db 419 NTQAAQKLKDXEVAFTWNLFAKKAKEKPPQ 448

RESULT 11
US-08-446-100-27
; Sequence 27, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
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; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
US-08-446-100-27

Query Match 31.5%; Score 981.5; DB 3; Length 454;
Best Local Similarity 43.6%; Pred. No. 8.9e-92;
Matches 196; Conservative 91; Mismatches 158; Indels 5; Gaps 4;

QY 137 EDCLYLNIVYAPARAPGDPQLPPVMVWIIHGGGLMVGAASYDGLAALAHENVVVVTIQYRLG 196
Db 1 EHCLYLNIVYAPADLTKKNLPPVMVWIIHGGGLMVGAASYDGLAALAHENVVVVTIQYRLG 60
QY 197 IFGFLSTDDSHARGNWGLLDQVAALRWQENIAAFGGDPGNVTLFGOSAGASISGLMMS 256
Db 61 IWGFFSTGDEHSRGNWGHLDQVAALRWQDNIAFSGNPGSVTIIFGSGAGSVSVLVLS 120
QY 257 PLASGLFHRAISQSGTALFRLFITSNPLK-VAKKVAHLACNHNSTQILVNCRLALSGTK 315
Db 121 FLAKNLFHRAISGVALTSVLVKGDKVPLAEQIAITAGCKTTTSAAMVHCLAQKTEEE 180
QY 316 VMRSVNMRFLOLNFORDPEEIIWMSFVVDGVVVDVLLVLTQGVSSVYLLGVNVL 375
Db 181 LLETTLKIGNSYLWYRETQRESHLLGTVIDGMLLKTPEELQRENFHTVPMVGINKQ 240
QY 376 EFNWLLP-YIMKFLPNRQAMEKETTITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEHDWK 434
Db 241 EFGWLLPQMLMSYPLSEGQDQKTAMSLGSPFLFAIAKELIPEATEKYLGGTD--DTV 298
QY 435 MLNRNMDIVODATFVYATLQTAHYHRDAGLPVLYIEFEHH-ARGIIVKPRDGDAGHDE 493
Db 299 KKKDLILDIAVDMFVPSVIVARNHRDAGAPTYMYEFQYRPFSSDMKPKTVIGDHGDE 358
QY 494 MYFLFGGPFATGLSMGKEKALSQMKMYANFARTGNPDGNLPCWPRYNKDEKYLQDF 553
Db 359 LFSVFGAPFLKEGASEEIEIRLSKVMKFWANFARNGNPKGLPHWPEYNQKEGYLQIGA 418
QY 554 TTRVGMKLEKKMAFMWSLYQSQRPEKORQ 583
Db 419 NTQAAQKLKDXEVAFTWNLFAKKAKEKPPQ 448

RESULT 12
US-08-446-100-28
; Sequence 28, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,100
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenna
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
```

```

; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-28

Query Match      31.4%; Score 977.5; DB 3; Length 454;
Best Local Similarity 43.6%; Pred. No. 2.3e-91;
Matches 196; Conservative 90; Mismatches 159; Indels 5; Gaps 4;

QY 137 EDCLYLVYAPARAPGDPQLPVWVFFGAFIVGAASSYEGSDLAAREKVLVFLQRLG 196
DB 1 EHCYLVNIYTPADLTCKNRLPVWVWIGHGLDVGAASYDGLALAAHENVVVTIQRLG 60

QY 197 IFGLSTDDSHARGNWGLLDQMAALRWQENIAAFGGDPGNVTLFGOSAGAMSISGLMS 256
DB 61 IWGFSTGDEHSRGNWGLDQVAALRWQDNIAAFGGNPGSVTFGESAGGESVSVLVLS 120

QY 257 PLASGLFHRAISQSGTALFRLFTSNPLK-VAKKVAHLACGNHNSQILVNCRLALSGTK 315
DB 121 PLAKNLFHRAISESGVALTSVLVKGDVLPKLAQIALTAGCKTTTSAAMVHCLRQKTEE 180

QY 316 VMRVSNKMRFLQNFQDPDEEIIWMSPPVVDGVVIPPDDPLVLLTQGVKSSVPYLLGVNLL 375
DB 181 LLETTLKIGNSYLTWYRETQRESTLLGTVDGMLLKTPEELQRENFHFTVPYVGVINKQ 240

QY 376 EFNWLLP-YIMKFFPLNQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNHDWK 434
DB 241 EFGWLIIPWQLMSYPLSEGQDDQKATMSLLGSPILFAIAKELIPEATEKYLGGTD--DTV 298

QY 435 MLNRNMDIVQDATFVYATLQTAHYHRDAGLPVLYVEFEHH-ARGIIVKPRTDGADHGE 493
DB 299 KKDLILDLIADVMFGVPSVIVARNHRDAGAPTYMYEFQYRPSFSSDMKPKTVIGDHGE 358

QY 494 MYFLFGGPPATGLSMGKEKALSQMKMYANPARTGNPDGNLPCWPRYNKDEKYLQDF 553
DB 359 LFSVFGAPFLKEGASEEIRLSKXVMKFWANFARNPNNGKGLPHWPEYNQKEGYLQIGA 418

QY 554 TTRVGMKLKKEKXAFWMSLYQSQRPEKQ 583
DB 419 NTQAAQKLKDEKAVAFWNLFAKXAVEKPPQ 448

```

## RESULT 13

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US-08-446-100-29
; Sequence 29, Application US/08446100
; Patent No. 6001625
; GENERAL INFORMATION:
; APPLICANT: Broomfield, Clarence A
; APPLICANT: Millard, Charles B
; APPLICANT: Lockridge, Oksana
; TITLE OF INVENTION: Site-Directed Mutagenesis of Esterases
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hendricks and Assoc.
; STREET: 9669 A Main Street, P.O. Box 2509
; CITY: Fairfax
; STATE: VA
; COUNTRY: US
; ZIP: 22031
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446.100
; FILING DATE: 19-May-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hendricks, Glenn
; REGISTRATION NUMBER: 32,535
; REFERENCE/DOCKET NUMBER: Broomfield
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 425-4250
; TELEFAX: (703) 425-2767
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ANTI-SENSE: YES
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: human esterases
; US-08-446-100-29

Query Match      31.4%; Score 977.5; DB 3; Length 454;
Best Local Similarity 43.6%; Pred. No. 2.3e-91;
Matches 196; Conservative 90; Mismatches 159; Indels 5; Gaps 4;

QY 137 EDCLYLVYAPARAPGDPQLPVWVFFGAFIVGAASSYEGSDLAAREKVLVFLQRLG 196
DB 1 EHCYLVNIYTPADLTCKNRLPVWVWIGHGLDVGAASYDGLALAAHENVVVTIQRLG 60

QY 197 IFGLSTDDSHARGNWGLLDQMAALRWQENIAAFGGDPGNVTLFGOSAGAMSISGLMS 256
DB 61 IWGFSTGDEHSRGNWGLDQVAALRWQDNIAAFGGNPGSVTFGESAGGESVSVLVLS 120

QY 257 PLASGLFHRAISQSGTALFRLFTSNPLK-VAKKVAHLACGNHNSQILVNCRLALSGTK 315
DB 121 PLAKNLFHRAISESGVALTSVLVKGDVLPKLAQIALTAGCKTTTSAAMVHCLRQKTEE 180

QY 316 VMRVSNKMRFLQNFQDPDEEIIWMSPPVVDGVVIPPDDPLVLLTQGVKSSVPYLLGVNLL 375
DB 181 LLETTLKIGNSYLTWYRETQRESTLLGTVDGMLLKTPEELQRENFHFTVPYVGVINKQ 240

QY 376 EFNWLLP-YIMKFFPLNQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNHDWK 434
DB 241 EFGWLIIPWQLMSYPLSEGQDDQKATMSLLGSPILFAIAKELIPEATEKYLGGTD--DTV 298

QY 435 MLNRNMDIVQDATFVYATLQTAHYHRDAGLPVLYVEFEHH-ARGIIVKPRTDGADHGE 493
DB 299 KKDLILDLIADVMFGVPSVIVARNHRDAGAPTYMYEFQYRPSFSSDMKPKTVIGDHGE 358

QY 494 MYFLFGGPPATGLSMGKEKALSQMKMYANPARTGNPDGNLPCWPRYNKDEKYLQDF 553
DB 359 LFSVFGAPFLKEGASEEIRLSKXVMKFWANFARNPNNGKGLPHWPEYNQKEGYLQIGA 418

QY 554 TTRVGMKLKKEKXAFWMSLYQSQRPEKQ 583
DB 419 NTQAAQKLKDEKAVAFWNLFAKXAVEKPPQ 448

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## RESULT 14

```

US-10-023-515-4
; Sequence 4, Application US/10023515
; Patent No. 6664091
; GENERAL INFORMATION:
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Silos-Santiago, Imaculada
; TITLE OF INVENTION: 53010, A NOVEL HUMAN CARBOXYLSTERASE
; TITLE OF INVENTION: FAMILY MEMBER AND USES THEREOF

```

FILE REFERENCE: 10448-122001  
CURRENT APPLICATION NUMBER: US/10/023,515  
CURRENT FILING DATE: 2001-12-18  
PRIOR APPLICATION NUMBER: 60/256,369  
PRIOR FILING DATE: 2000-12-18  
PRIOR APPLICATION NUMBER: 60/279,508  
PRIOR FILING DATE: 2001-03-28  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4  
LENGTH: 574  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Consensus sequence  
US-10-023-515-4

Query Match 29.2%; Score 908.5; DB 4; Length 574;  
Best Local Similarity 39.6%; Pred. No. 4.1e-84;  
Matches 226; Conservative 87; Mismatches 181; Indels 77; Gaps 24;  
Db 24;  
67 GKTPIQVFLGVPSRPLGLIRAPPPEPPEPKGIRDATYPPGCLQ-ESWG-QLASMY 123  
13 GEOSVSYFLGIPAEPPVGNLRKAPQYKEPKSDVLDATKYPPSCLODDDFGSLDLK 72  
124 VSTR-----ERYKWLRFSEDCLYLVNYPARAPGDPQLPVMWFFGGAPIVGAAS--- 174  
73 VALKGLSLGNKLVGLKSLDCLYLVNYPKNTKPKNSKLPVMWVIRGGGFMFGSHSLPL 132  
175 --YEGSLAAREKVLVFLQHRIGIFGLSTDDSH--ARGNWGLDQMAALRWVQENIAA 230  
133 SLVDGSLAREGNVIVVINSYIRGLPGLSTGDKLPFGSGNYGLLQRLAKVQDNIAA 192  
231 FGDGPGNVTLFGSAGAMSISGLMMS-----PLASGLFHRAISQSGTAL--FRLFITSN 282  
193 FGDGPNVSTIFGESAGAASVSLLLSNGGDNPPSSKGLFHRAISQSGSALLSPWAIQSEN 252  
283 PLKVAKVVAHLAGNHNSTQILNCLRALSGTKVMRVSNKMRFLQNFQDPP--EELIWSM 341  
253 ARGRAKELARLLGNETSSSELDDCLRSKSAEELLEATRSF---LFEVVPFLPLFLAP 308  
342 SPVVDG---VTPDDPLVLTQGVSVSPYLLGVNVLNLFNMLLPYIMKFFPLNRQA--- 393  
309 GPVVDGDDAPEAFPEDEPEELIKEGKPADVPYLLIGVTKDEGG---YFAAMLLNASKGE 364  
394 --MKET-----ITKMLNSTLTLLNIKEQVPL---VVEYLDNVNHEHDKMLNRM 440  
365 DELKKTNPDPVWLELLKYLFLFYASEALNI-KDMDDLADKVLKYPGVDVDDFSVESRKNL 423  
441 MDIVQDATEVYATLQTAHYH-RDAGLPVLYFEFEHAR-GI-----IVKPRTDGADHGD 492  
424 QDMLTDLFLKCPTRVAADLHAKHGSPVYAVVFDHPASFGIGQFLAKRVDPFEGGAVHGD 483  
493 EMYFLFGGPPFAT---GLSMGKEKALSQMMKYWANFARTGNPNNDG---NLPCWPRYNKD 545  
484 EIFFVFGNPLLEQLYKATEBEESKSSKTMNYWANFARTGNPNNGTNGSLVVMKPYTSE 543  
546 E-KY-LQDFTTRVMKLEKKK-----MAFW 569  
544 EQVSLILLTITTAQKLKARDPRKVLNCFW 574

RESULT 15  
US-09-491-356C-21  
Sequence 21, Application US/09491356C  
Patent No. 6566061  
GENERAL INFORMATION:  
APPLICANT: Philibert, Robert A.  
APPLICANT: Ginn, Edward I.  
APPLICANT: Delisi, Lynn  
TITLE OF INVENTION: IDENTIFICATION OF POLYMORPHISMS IN THE PCTG4 REGION OF XQ13  
FILE REFERENCE: 9465.6US11  
CURRENT APPLICATION NUMBER: US/09/491,356C

CURRENT FILING DATE: 2000-01-26  
PRIOR APPLICATION NUMBER: PCT/US99/09365  
PRIOR FILING DATE: 1999-04-29  
PRIOR APPLICATION NUMBER: 60/083,465  
PRIOR FILING DATE: 1998-04-29  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 21  
LENGTH: 836  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-09-491-356C-21  
Query Match 27.3%; Score 849; DB 4; Length 836;  
Best Local Similarity 33.2%; Pred. No. 1e-77;  
Matches 215; Conservative 92; Mismatches 191; Indels 150; Gaps 21;  
Db 21;  
30 WSLTLCIM---AO-----TALGALHTKR-POVVTYKTYGLQKQKMHVGT 69  
2 WLLALCLVLAGAGRGGGPGGAPGPGGLGSLGSEERFPVNTAYGRVGRVERELNNE 61  
70 ---PIQVFLGVPSRPLGLIRAPPPEPPEPKGIRDATYPPGCLQESWQQL----- 119  
62 ILGPVVQFLGVYATPPLGARRFQPEAPASWPGVRNATTLPPACPNLHGALPAIMLPV 121  
120 -----ASMVSTREYKWLRFSEDCLYLVNYPAR-----APGDPQL-- 156  
122 WFTDNLEAAATYVQHQ-----SEDCLYLVNLYVPTEDGPLTKKROBATLNPPTDIRD 173  
157 ---PMTWFFPGGAFIVGAASYESGSLAAREKVLVFLQHRIGIFGLSTDDSHARGNW 212  
174 SGKPFVFLFHGGSTWEGTGNMFGSVLAAYGNVIVATLNYRLGVGLSTGDOAAKGY 233  
213 GLDDQMAALRWVQENIAAFGGDGNVTLFGSAGAMSISGLMMSPLASGLFHRAISQSGT 272  
234 GLDDQIALRMLSENIHAFGGDPERITIFGSGAGASCNVLLILSHHSEGLFQKALAQSGT 293  
273 ALFRLFITSNPLKVAKVVAHLAGNHNSTQILNCLRALSGTKVMRVSNKMRFLQNFQR 332  
294 AISSNVNYPKLYTRLLAAKVGCDREDSTEAVECLRRKSSREL-----VDQDV 342  
333 DPEEIIWMSVVDGVVIPPDDPLVLTQGVSVSPYLLGVNVLNLE----- 376  
343 QPARYHIAFGPVVDGVVDPDDPEILMQQGEFLNYDMLIGVNGQEGKLVESDAESDGV 402  
377 ---FNW---LLPYIMKFPNLRQAKRKETITKMLNSTLTLLNITKEQVPLVVEEYLDNVN 429  
403 ASAFDFTVSNFVNDLYGYPEGKDVLR-ETIKFM-----YTDWAD 440  
430 EHDWKMLNRNMDIVQDATEVYATLQTAHYHREDAGLPVLYFEFEH--ARGIIVKPRTDG 487  
441 RDNEMERRKTLLALFTDQWVAPAVATAKLHADYQSPVYFTFYHHCQAE--RPEWAD 497  
488 ADHGDEMIFLFGGPPF---ATGL---SMGK-EKALSQMMKYWANFARTGNPDGNLP---- 537  
498 AAAGDELVPVFGVPMVVGATDLPFCNFSKNDVMSLAVVTYNTWNTFAKTGDPNQ-PVPQDTK 556  
538 -----CWPRYN-KDEKYLQDFTTRVGMKLEKKQKQVAFWMSL 572  
557 FIHTKENREFEVWVSKFNSKEQYLHGLKPRVRDNYRANKVAFWLEL 604

Search completed: August 3, 2004, 22:29:22  
Job time : 20 secs





QY 181 AAREKVVLFVQLHRLGIFGFLSTDDSHARGNWGLDDMAALRWVOENIAAAGGDPGNVTL 240  
DB 181 AAREKVVLFVQLHRLGIFGFLSTDDSHARGNWGLDDMAALRWVOENIAAAGGDPGNVTL 240  
QY 241 FQSAGAMSISGLMWSPLASGLFHRAISQSCTALFRLITSNPLKVAKVVAHLACGNHNS 300  
DB 241 FQSAGAMSISGLMWSPLASGLFHRAISQSCTALFRLITSNPLKVAKVVAHLACGNHNS 300  
QY 301 TQILVNCRLALSGTKVMRSNKRFLQNFORDPEEIIWSMSPVVDGVVIPPDDPLVLTQ 360  
DB 301 TQILVNCRLALSGTKVMRSNKRFLQNFORDPEEIIWSMSPVVDGVVIPPDDPLVLTQ 360  
QY 361 GKVSVPYLLGVNNEFNWLLPYIMKFPINRQAMRKETITKQMLWSTRTLLNITKEQVPLV 420  
DB 361 GKVSVPYLLGVNNEFNWLLPYIMKFPINRQAMRKETITKQMLWSTRTLLNITKEQVPLV 420  
QY 421 VEEYLDNNEHDWKLNRNMMDIVQDATFVYATLQTAHYHRDAGLPVLYFEFHARGII 480  
DB 421 VEEYLDNNEHDWKLNRNMMDIVQDATFVYATLQTAHYHRDAGLPVLYFEFHARGII 480  
QY 481 VKPRTDGDHGDENYFLFGGPFATGLSMGKEKALSQMKYWANFARTGNPDGNLPCWP 540  
DB 481 VKPRTDGDHGDENYFLFGGPFATGLSMGKEKALSQMKYWANFARTGNPDGNLPCWP 540  
QY 541 RYNKDEKYLQDFTTRVGMKLEKKMAFWMSLYQSQRPEKORQF 584  
DB 541 RYNKDEKYLQDFTTRVGMKLEKKMAFWMSLYQSQRPEKORQF 584

## RESULT 2

US-10-343-593-10  
; Sequence 10, Application US/10343593  
; Publication No. US20040110259A1  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.; BAUGHN, Mariah R.;  
; APPLICANT: BRUNS, Christopher M.; DAS, Debopriya;  
; APPLICANT: DELEGANE, Angelo M.; DING, Li;  
; APPLICANT: ELLIOT, Vicki S.; GANDHI, Ameena R.;  
; APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.;  
; APPLICANT: KHAN, Farrah A.; LAL, Preeti G.;  
; APPLICANT: LEE, Sally; LU, Dyung Aina M.;  
; APPLICANT: LU, Yan; ARVIZU, Chandra S.;  
; APPLICANT: RAMKUMAR, Jayalaxmi; RING, Huijun Z.;  
; APPLICANT: SANJAYWALA, Madhusudan M.; TANG, Y. Tom;  
; APPLICANT: THANGAVELU, Kavitha; THORNTON, Michael;  
; APPLICANT: TRIBOULEY, Catherine M.; CHAWLA, Narinder K.;  
; APPLICANT: WARREN, Bridget A.; YANG, Junning;  
; APPLICANT: YAO, Monique G.; YUE, Henry  
; TITLE OF INVENTION: DRUG METABOLIZING ENZYMES  
; FILE REFERENCE: PI-0185 USN  
; CURRENT APPLICATION NUMBER: US/10/343,593  
; CURRENT FILING DATE: 2003-01-29  
; PRIOR APPLICATION NUMBER: US 60/223,055  
; PRIOR FILING DATE: 2000-08-04  
; PRIOR APPLICATION NUMBER: US 60/224,728  
; PRIOR FILING DATE: 2000-08-11  
; PRIOR APPLICATION NUMBER: US 60/226,440  
; 2000-08-18  
; PRIOR APPLICATION NUMBER: US 60/228,067  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/230,063  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: US 60/232,244  
; PRIOR FILING DATE: 2000-09-13  
; PRIOR APPLICATION NUMBER: US 60/234,269  
; PRIOR FILING DATE: 2000-09-20  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PERL Program  
; SEQ ID NO 10  
; LENGTH: 584  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:

; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 7478588CD1  
US-10-343-593-10

Query Match 100.0%; Score 3112; DB 16; Length 584;  
Best Local Similarity 100.0%; Pred. No. 2.5e-289;  
Matches 584; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MESTVLPSTVLSLPTAGAGWSMWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTQ 60  
DB 1 MESTVLPSTVLSLPTAGAGWSMWILCWSLTLCLMAQTALGALHTKRPQVVTKYGTQ 60  
QY 61 GKQMHVGKTIQOVFLGVFPFSPPLGLILRFAPPEPPKGIKRDATYPPGCLQESWGOLA 120  
DB 61 GKQMHVGKTIQOVFLGVFPFSPPLGLILRFAPPEPPKGIKRDATYPPGCLQESWGOLA 120  
QY 121 SMYVSTRERYKWLRFSEDCLYLVNYPAPAPGDPQPLPVMWFFPGAFIVGAASVEGSDL 180  
DB 121 SMYVSTRERYKWLRFSEDCLYLVNYPAPAPGDPQPLPVMWFFPGAFIVGAASVEGSDL 180  
QY 181 AAREKVVLFVQLHRLGIFGFLSTDDSHARGNWGLDDMAALRWVOENIAAAGGDPGNVTL 240  
DB 181 AAREKVVLFVQLHRLGIFGFLSTDDSHARGNWGLDDMAALRWVOENIAAAGGDPGNVTL 240  
QY 241 FQSAGAMSISGLMWSPLASGLFHRAISQSCTALFRLITSNPLKVAKVVAHLACGNHNS 300  
DB 241 FQSAGAMSISGLMWSPLASGLFHRAISQSCTALFRLITSNPLKVAKVVAHLACGNHNS 300  
QY 301 TQILVNCRLALSGTKVMRSNKRFLQNFORDPEEIIWSMSPVVDGVVIPPDDPLVLTQ 360  
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QY 361 GKVSVPYLLGVNNEFNWLLPYIMKFPINRQAMRKETITKQMLWSTRTLLNITKEQVPLV 420  
DB 361 GKVSVPYLLGVNNEFNWLLPYIMKFPINRQAMRKETITKQMLWSTRTLLNITKEQVPLV 420  
QY 421 VEEYLDNNEHDWKLNRNMMDIVQDATFVYATLQTAHYHRDAGLPVLYFEFHARGII 480  
DB 421 VEEYLDNNEHDWKLNRNMMDIVQDATFVYATLQTAHYHRDAGLPVLYFEFHARGII 480  
QY 481 VKPRTDGDHGDENYFLFGGPFATGLSMGKEKALSQMKYWANFARTGNPDGNLPCWP 540  
DB 481 VKPRTDGDHGDENYFLFGGPFATGLSMGKEKALSQMKYWANFARTGNPDGNLPCWP 540  
QY 541 RYNKDEKYLQDFTTRVGMKLEKKMAFWMSLYQSQRPEKORQF 584  
DB 541 RYNKDEKYLQDFTTRVGMKLEKKMAFWMSLYQSQRPEKORQF 584

## RESULT 3

US-09-978-295A-254  
; Sequence 254, Application US/09978295A  
; Patent No. US20020156006A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.



APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
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 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085580  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085573  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085704  
 PRIOR FILING DATE: 1998-05-15  
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 65.1%; Score 2026.5; DB 9; Length 545;  
 Best Local Similarity 80.3%; Pred. No. 3.6e-185;  
 Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;  
 6 LPSVLPBLLPTAGACGMRILCWSLTCLMAOTAGLHTRPQVTKYKGLQKQKH 65  
 47 LGSTTPATTSAFSGFGTGLGKPKATFTLGTGNTGALHTRPQVTKYKGLQKQKH 106  
 66 VKTPIQVFLGVFSPRPPLILRPAPEPPPEPKGIRDAITPPGKSLALSPGMSAVAS 166  
 107 VKTPIQVFLGVFSPRPPLILRPAPEPPPEPKGIRDAITPPGKSLALSPGMSAVAS 166  
 111 -----CLOESWGQASVMVSTRERYKWLRFSEDCLYNY 145  
 167 RLATASRVSQASLLPQLSVMGYRC-QESWGQASVMVSTRERYKWLRFSEDCLYNY 226  
 146 APARAPGPPQLPVMVFPFGAFIVGAASSYEGSDLAAREKVLVFLQHRIGIFGLSTDD 205  
 227 APARAPGPPQLPVMVFPFGAFIVGAASSYEGSDLAAREKVLVFLQHRIGIFGLSTDD 286  
 206 SHARGNWGLLQMAALRWQENIAAFGDPQNVTLFQOSAGAMISGLMWSPLASGLFHR 265  
 287 SHARGNWGLLQMAALRWQENIAAFGDPQNVTLFQOSAGAMISGLMWSPLASGLFHR 346  
 266 AISOQSTALFRLFTSNPKVAKVAHLAGCNHNSITVLNCLRALSGTKMVSVMKMF 325  
 347 AISOQSTALFRLFTSNPKVAKVAHLAGCNHNSITVLNCLRALSGTKMVSVMKMF 406  
 326 LQINFORPELILMSVWGVVIPPDPVLLTQGVSSVPYLLGVNNLEFNWLLPYIM 385  
 407 LQINFORPELILMSVWGVVIPPDPVLLTQGVSSVPYLLGVNNLEFNWLLPY-- 464  
 386 KPPLNRQMRKETITKMLWSTRLNLTKEQVPLVVEEYLDNVDNNEHDKWLRNMDIVQ 445  
 465 -----NITKEQVPLVVEEYLDNVDNNEHDKWLRNMDIVQ 499  
 446 DATFYATLQAHVHRD 462  
 500 DATFYATLQAHVHRE 516

RESULT 4  
 US-09-978-697-254  
 ; Sequence 254, Application US/09978697  
 ; Patent No. US20020169284A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerber, Hanspeter  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, J. Christopher  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Kljavin, Ivar J.  
 ; APPLICANT: Kuo, Sophia S.  
 ; APPLICANT: Napier, Mary A.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; APPLICANT: Roy, Margaret Ann  
 ; APPLICANT: Shelton, David L.  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Williams, P. Mickey  
 ; APPLICANT: Wood, William I.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2630P1C27  
 ; CURRENT APPLICATION NUMBER: US/09/978,697  
 ; CURRENT FILING DATE: 2001-10-16  
 ; PRIOR APPLICATION NUMBER: 09/918585  
 ; PRIOR FILING DATE: 2001-07-30  
 ; PRIOR APPLICATION NUMBER: 60/062250  
 ; PRIOR FILING DATE: 1997-10-17  
 ; PRIOR APPLICATION NUMBER: 60/064249  
 ; PRIOR FILING DATE: 1997-11-03  
 ; PRIOR APPLICATION NUMBER: 60/065311  
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Query Match 65.1%; Score 2026.5; DB 9; Length 545;  
Best Local Similarity 80.3%; Pred. No. 3.6e-185;  
Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

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Dd 47 LGSTSTPATTSPSSGFGTGLFGSPATGFTLGGTNTGALHTKRPQVVTKYGTLOGKQVH 106  
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Dd 107 VGKTPIQVFLGVFSPRPPLGILRFPAPPPEPPPEPKGIRDTATYPPGWSLALSEFNSAVARS 166  
QY 111 -----CLOESWCOLASMYVSTREYKWLRFSEDCLYLVNY 145  
Dd 167 RLTAATSASRVQASLLPQPLSVWGVYRCLQESWCOLASMYVSTREYKWLRFSEDCLYLVNY 226

Qy	146	APAPGPDQ	PLVMVWF	PGGAFI	VCAASSY	EGSDLAARE	KVVLVFLQ	HRIGIFG	FLSTDD	205	
Db	227	APAPGPDQ	PLVMVWF	PGGAFI	VCAASSY	EGSDLAARE	KVVLVFLQ	HRIGIFG	FLSTDD	286	
Qy	206	SHARGNWGLL	DQMAALR	VQWENIA	AFGGDP	GNVTLFG	CSAGAMS	ISGLMMS	PLASGLFHR	265	
Db	287	SHARGNWGLL	DQMAALR	VQWENIA	AFGGDP	GNVTLFG	CSAGAMS	ISGLMMS	PLASGLFHR	346	
Qy	266	AISQSGTAL	FRUFITS	NPLKVA	KVAHLAG	CNNHSTQ	ILVNC	LALSGT	KWVRVSNKMF	325	
Db	347	AISQSGTAL	FRUFITS	NPLKVA	KVAHLAG	CNNHSTQ	ILVNC	LALSGT	KWVRVSNKMF	406	
Qy	326	LQNLNCRQ	DEPEEII	WSNS	PWDGVV	IPDDPLV	LLTQ	GKVSSVP	YLLGVNNLEFNWLLPYTM	385	
Db	407	LQNLNCRQ	DEPEEII	WSNS	PWDGVV	IPDDPLV	LLTQ	GKVSSVP	YLLGVNNLEFNWLLPY--	464	
Qy	386	KPFLNQR	AMKETIT	KMLWS	RTLLNTT	KEQVPLV	VEEYLD	NVNEDH	WKLRNRMMDIVQ	445	
Db	465	-----	-----	-----	-----	NITKEQ	VPLV	VEEYLD	NVNEDH	WKLRNRMMDIVQ	499
Qy	446	DATFVYAT	LOTAHYHRD	462							
Db	500	DATFVYAT	LOTAHYHRE	516							

## RESULT 5

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US-978-192A-254
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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
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; APPLICANT: Gurney, Austin L.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC9
; CURRENT APPLICATION NUMBER: US/09/978.192A
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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; PRIOR FILING DATE: 1997-10-17
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Db 287 SHARGNWGLDQMAALRWQENIAAFGGDPGNVTLFGOSAGAMISGLMWSPLASGLPFR 346  
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; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
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APPLICANT: Tumas, Daniel  
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APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
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Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

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66 VGKTPIQVFLGVPSRPLGILRAPPEPEPKWIRDAITYPPG----- 110
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206 SHARGNWGLLDOMAALEHWQENIAAFGGDPGNVTLFGQSAGAMISGLMWSPLASGLFHR 265
287 SHARGNWGLLDOMAALEHWQENIAAFGGDPGNVTLFGQSAGAMISGLMWSPLASGLFHR 346
266 AISQSGLTALFLFTTSNPLKVAKVVAHLACGNHNSQTQLVNCFLALSGTKVMRVSNKORF 325
347 AISQSGLTALFLFTTSNPLKVAKVVAHLACGNHNSQTQLVNCFLALSGTKVMRVSNKORF 406
326 LQNFQRPDEIIVMSMSPVGVVIPPDPVLLTQGVKSSVPYLLGVNNLEFNWLLPYIM 385
407 LQNFQRPDEIIVMSMSPVGVVIPPDPVLLTQGVKSSVPYLLGVNNLEFNWLLPY-- 464
386 KFFPLNRQMRKETITKMLWSTRLNITKEQVPLVWEYLDNVNEHDWKMLRNRMDIVQ 445
465 -----NITKEQVPLVWEYLDNVNEHDWKMLRNRMDIVQ 499
446 DATFVYATLQTAHYHRE 462
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DB 500 DATFVYATLQTAHYHRE 516
RESULT 7
US-09-978-189-254
Sequence 254, Application US/09978189
Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrata, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Foag, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas P.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
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PRIOR FILING DATE: 1998-03-10
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PRIOR APPLICATION NUMBER: 60/077641
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PRIOR APPLICATION NUMBER: 60/077791
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; PRIOR FILING DATE: 1998-03-26  
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 ; PRIOR APPLICATION NUMBER: 60/085573  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085704  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 65.1%; Score 2026.5; DB 10; Length 545;  
 Best Local Similarity 80.3%; Pred. No. 3.6e-185;  
 Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

Oy	6	LPSTVLPSSLPTAGAGWSRWILCWSLTLCLMACTALGALHTKRPQVTKYGTLOGQKH	65
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Db	47	LGSTSTPATTSAPSSGFGTCLFQSKATGTTGGTNGALHTKRPQVTKYGTLOGQKH	106
		:	
Oy	66	VGKTPIQVFLGVFPSPPLGILFAPPEPPKWKIRDATTPPG	110
		:	
Db	107	VGKTPIQVFLGVFPSPPLGILFAPPEPPKWKIRDATTPPGWSLSPGWSAVERS	166
		:	
Oy	111	-----CLQBSWGQLASMYSTRERYKWLRFSEDCLYLVY	145

Query Match 65.1%; Score 2026.5; DB 10; Length 545;  
Best Local Similarity 80.3%; Pred. No. 3.6e-185; Indels 67; Gaps 2;  
Matches 399; Conservative 5; Mismatches 26;  
QY 6 LPSTVLPSSLPTACAGSMRWILCWSLTLCLMAQTALGALHTKRPQVVTYKGTLOGKQWH 65  
Db 47 LGSTSPATTSAPSSGFGTGLFGSKPATGFTLGGTNTGALHTKRPQVVTYKGTLOGKQWH 106  
QY 66 VGTPTQVFLGVDFSPDPLGILRPAPEPPEPKWGIKRDATTTPPG----- 110  
Db 107 VGKTPQVFLGVDFSPDPLGILRPAPEPPEPKWGIKRDATTTPPGWSLALSPGWSAVARS 166  
QY 111 -----CLQESWGQLASMYVSTRERYKWLRFSEDCLYLNVY 145  
Db 167 RLATASASRVQASLLPQLSVNGYRCLOESWGQLASMYVSTRERYKWLRFSEDCLYLNVY 226  
QY 146 APARAPGDPOLPVMVWFFGGAFIVGAASSYEGSDLAAREKVLVFLQHRLGIFGLSTDD 205  
Db 227 APARAPGDPOLPVMVWFFGGAFIVGAASSYEGSDLAAREKVLVFLQHRLGIFGLSTDD 286  
QY 206 SHARGNWGLLDQAAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR 265  
Db 287 SHARGNWGLLDQAAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR 346  
QY 266 AISQSGTALFRLFITSNPLKVAKVVAHLACNHNSTQILVNCRLALSGTKVMRVSNKORF 325  
Db 347 AISQSGTALFRLFITSNPLKVAKVVAHLACNHNSTQILVNCRLALSGTKVMRVSNKORF 406  
QY 326 LQINFORDEEIIWMSPPVVDGVPDPLVLLTQGVSSVPYLLGVNNLEFNWLLPYIM 385  
Db 407 LQINFORDEEIIWMSPPVVDGVPDPLVLLTQGVSSVPYLLGVNNLEFNWLLPY-- 464  
QY 386 KFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNHDWKLNRNMMDIVQ 445  
Db 465 -----NITKEQVPLVVEEYLDNVNHDWKLNRNMMDIVQ 499  
QY 446 DATFYATLQTAHYHRD 462  
Db 500 DATFYATLQTAHYHRE 516

RESULT 9  
US-09-978-585A-254  
; Sequence 254, Application US/09978585A  
; Publication No. US20030049633A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.

Db 167 RLATASASRVQASLLPQLSVNGYRCLOESWGQLASMYVSTRERYKWLRFSEDCLYLNVY 226  
QY 146 APARAPGDPOLPVMVWFFGGAFIVGAASSYEGSDLAAREKVLVFLQHRLGIFGLSTDD 205  
Db 227 APARAPGDPOLPVMVWFFGGAFIVGAASSYEGSDLAAREKVLVFLQHRLGIFGLSTDD 286  
QY 206 SHARGNWGLLDQAAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR 265  
Db 287 SHARGNWGLLDQAAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR 346  
QY 266 AISQSGTALFRLFITSNPLKVAKVVAHLACNHNSTQILVNCRLALSGTKVMRVSNKORF 325  
Db 347 AISQSGTALFRLFITSNPLKVAKVVAHLACNHNSTQILVNCRLALSGTKVMRVSNKORF 406  
QY 326 LQINFORDEEIIWMSPPVVDGVPDPLVLLTQGVSSVPYLLGVNNLEFNWLLPYIM 385  
Db 407 LQINFORDEEIIWMSPPVVDGVPDPLVLLTQGVSSVPYLLGVNNLEFNWLLPY-- 464  
QY 386 KFPLNRQAMRKETITKMLWSTRTLLNITKEQVPLVVEEYLDNVNHDWKLNRNMMDIVQ 445  
Db 465 -----NITKEQVPLVVEEYLDNVNHDWKLNRNMMDIVQ 499  
QY 446 DATFYATLQTAHYHRD 462  
Db 500 DATFYATLQTAHYHRE 516

RESULT 8  
US-09-978-608A-254  
; Sequence 254, Application US/09978608A  
; Publication No. US20030045462A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
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; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P26301C22  
; CURRENT APPLICATION NUMBER: US/09/978.608A  
; CURRENT FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 254  
; LENGTH: 545  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-978-608A-254

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C5
; CURRENT APPLICATION NUMBER: US/09/978.585A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 254
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-978-585A-254

Query Match          65.1%; Score 2026.5; DB 10; Length 545;
Best Local Similarity 80.3%; Pred. No. 3.6e-185;
Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

QY 6 LPSTVLSLLPTAGAGSMRWILCWSLTLCLMAQTALGALHTKRPQVWTKYGLQKQKH 65
DB 1 LGSTSTPATTSAPSSGFGTGLPGSKPATGFTLGCTNTGALHTKRPQVWTKYGLQKQKH 106
QY 66 VGTPIQVFLGVPSRPLGLIRFAPPEPEPKGIRDATTTPPG----- 110
DB 107 VGTPIQVFLGVPSRPLGLIRFAPPEPEPKGIRDATTTPPGWSLSPGWSAVARS 166
QY 111 -----CLQBSWGQLASMYVSTREYKWLRFSEDCLYLVNY 145
DB 167 RLATSASRVQASLLPQLSVWGYRCLOBSWGQLASMYVSTREYKWLRFSEDCLYLVNY 226
QY 146 APARAPGDPOLPMWPFPGAFIVGAASSYEGSDLAAREKVLVFIQHLRIGFGLSTDD 205
DB 227 APARAPGDPOLPMWPFPGAFIVGAASSYEGSDLAAREKVLVFIQHLRIGFGLSTDD 286
QY 206 SHARGNWGLLDQAAALRWQENIAAFGGDPGNVTLFGQAGAGMSISGLMWSPLASGLFHR 265
DB 287 SHARGNWGLLDQAAALRWQENIAAFGGDPGNVTLFGQAGAGMSISGLMWSPLASGLFHR 346
QY 266 AISQSGTALFRLPITSNPLKVAKVLAHAGCNHNSQILVNCCLRALSGTKVNRVSNKWRP 325
DB 347 AISQSGTALFRLPITSNPLKVAKVLAHAGCNHNSQILVNCCLRALSGTKVNRVSNKWRP 406
QY 326 LQNFORDPEELIWSPPVVDGVPVDDPLVLTQKSSVYLLGVNLEPNWLLPYIM 385
DB 407 LQNFORDPEELIWSPPVVDGVPVDDPLVLTQKSSVYLLGVNLEPNWLLPY-- 464
QY 386 KFFLNQAMRKETITKMLWSTRLNITKEQVPLVVEEYLDVNVNHDWMLNRNMMDIVQ 445
DB 465 -----NITKEQVPLVVEEYLDVNVNHDWMLNRNMMDIVQ 499
QY 446 DATEVYATLOTAYHRD 462
DB 500 DATEVYATLOTAYHRE 516

RESULT 10
US-09-978-191A-254
; Sequence 254, Application US/09978191A
; Publication No. US20030050239A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher

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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kluvin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas P.
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C4
; CURRENT APPLICATION NUMBER: US/09/978.191A
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; PRIOR FILING DATE: 1998-04-09
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081817
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      65.1%; Score 2026.5; DB 10; Length 545;
Best Local Similarity 80.3%; Pred. No. 3.6e-185;
Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

QY      6 LPSTVLPSPLLPTAGAGMSRWILCWSLTLCLMAQATLALHTKRPQVVTYKTLQSQMH 65
      47 LGSTSTPATTSAFSSGGTGLFGSKPATGTGLGTNTGALHTKRPQVVTYKTLQSQMH 106
      66 VGKTPIQVFLGVFSPRPPLGILRAPPEPPEPWKGRDATTYPPG----- 110
      107 VGKTPIQVFLGVFSPRPPLGILRAPPEPPEPWKGRDATTYPPGWSLALSPGWSAVARS 166
      111 -----CLQESWGOLASMYVSTRERYKWLRTSEDCLYLNRY 145
      167 RLATASASRVOASLLPQLSVWGYRCLQESWGOLASMYVSTRERYKWLRTSEDCLYLNRY 226
      146 APARAPGDPQLPVMVWPPGGAFIVGAASSYEGSDLAAREKVLVFLQHRLGIFGFLSTDD 205
      227 APARAPGDPQLPVMVWPPGGAFIVGAASSYEGSDLAAREKVLVFLQHRLGIFGFLSTDD 286
      206 SHARGNWGLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR 265
      287 SHARGNWGLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMMSPLASGLFHR 346
      266 AISQSGTALFRLFITSNPLKVAKVAHLAGCNHNSTQILVNCRLALSGTKVMRYSNRKF 325
      347 AISQSGTALFRLFITSNPLKVAKVAHLAGCNHNSTQILVNCRLALSGTKVMRYSNRKF 406
      326 LQALNFORDPBEI IWSNPFVVDGVIPDDPLVLLTQGVSSVPLLGVNNLEFNWLLPYIM 385
      407 LQALNFORDPBEI IWSNPFVVDGVIPDDPLVLLTQGVSSVPLLGVNNLEFNWLLPY-- 464
      386 KFPLNRQAMRKETITKMLWSTRLNITKXQVPLVVEEYLDNVNHDWKMLRNRMDIVQ 445
      465 -----NITKXQVPLVVEEYLDNVNHDWKMLRNRMDIVQ 499

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QY 446 DATFVYATLOTAYHRD 462  
Db 500 DATFVYATLOTAYHRE 516

RESULT 11  
US-09-978-403A-254  
; Sequence 254, Application US/09978403A  
; Publication No. US20030050240A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC17  
; CURRENT APPLICATION NUMBER: US/09/978,403A  
; CURRENT FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 65.1%; Score 2026.5; DB 10; Length 545;

Best Local Similarity 80.3%; Pred. No. 3.6e-185;

Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

QY 6 LPTVLPSLLPTAGAGSNRWILCSLTLCMAQTALGNLHTRKPPQVVTKYGTLOGKQMH 65
DB :|:
47 LGSTPFAITSPSSFGTGLFGSKPATGFTGGTNGTGAHTRKPPQVVTKYGTLOGKQMH 106
QY 66 VGTKPIQVGLVFPFRPPLGIIRFAPPEPPPEPWKGIROATTYPPG----- 110
DB :|:
107 VGTKPIQVGLVFPFRPPLGIIRFAPPEPPPEPWKGIROATTYPPGWSLALSPGWSAVARS 166
QY 111 -----CLOESWGQLASMYVSTRERYKWLRFSEDCLYLNVY 145
DB :|:
167 RLATASASRVQASLLFPQLSVNGYRCLOESWGQLASMYVSTRERYKWLRFSEDCLYLNVY 226
QY 146 APARAPGDPQLPVMWFFPGAFIVGAASYEGSDLAAREKVVLFQHRLGIFGFLSTDD 205
DB :|:
227 APARAPGDPQLPVMWFFPGAFIVGAASYEGSDLAAREKVVLFQHRLGIFGFLSTDD 286
QY 206 SHARGNWGLDQMAALRWVQENIAAFGGDPGNVTLFGSAGAMSTISGLMMSPLASGLFHR 265
DB :|:
287 SHARGNWGLDQMAALRWVQENIAAFGGDPGNVTLFGSAGAMSTISGLMMSPLASGLFHR 346
QY 266 AISOQTALFRFITSNPLKVAKKVAHLAGCHNHNSTQILLVNCRLSALSGTKVMRVSNKGRF 325
DB :|:
347 AISOQTALFRFITSNPLKVAKKVAHLAGCHNHNSTQILLVNCRLSALSGTKVMRVSNKGRF 406
QY 326 LQINFORDEEIIWMSPPVVDGVVIPPDPPLVLLTQGVSSVPYLLGVNNLEFNWLLPYIM 385
DB :|:
407 LQINFORDEEIIWMSPPVVDGVVIPPDPPLVLLTQGVSSVPYLLGVNNLEFNWLLPY-- 464
QY 386 KPEPLNQMRKETITKQMLNSTRLNITKEQVPLVVEEYLDNVNEDHDKMLNRNMDIVQ 445
DB :|:
465 -----NITKEQVPLVVEEYLDNVNEDHDKMLNRNMDIVQ 499
QY 446 DATEFVYATLQTAHYHRD 462
DB :|:
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RESULT 13

US-09-999-833A-254
; Sequence 254, Application US/09999833A
; Publication No. US20030054405A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1G65
; CURRENT APPLICATION NUMBER: US/09/999,833A
; PRIOR FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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 ; PRIOR APPLICATION NUMBER: 60/085573  
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 ; PRIOR APPLICATION NUMBER: 60/085704  
 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 65.1%; Score 2026.5; DB 10; Length 545;

Best Local Similarity 80.3%; Pred. No. 3.6e-185;  
Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

Qy	6	LPSTVLPSLLPTAGAGWNRWILCWSLTLCMAQTALGALHTKRPQVTKYGTLOGKQMH	65
Db	47	LGSTSTPATTSAPSSGFGTGLFGSKPATGFTLGCTNTGALHTKRPQVTKYGTLOGKQMH	106
Qy	66	VGXTPIQVFLGVFPFRPPLGILRFAPPEPPEPWKGRDATTYPPG	110
Db	107	VGXTPIQVFLGVFPFRPPLGILRFAPPEPPEPWKGRDATTYPPGWSLALSPQWSAVERS	166
Qy	111	-----CLOESWGOLASMYSTERYKWLRFSDCLYLVNY	145
Db	167	RLTATSASRVQASLLPQLSVWGYRCLQESWGOLASMYSTERYKWLRFSDCLYLVNY	226
Qy	146	APARAFGDPQLPVMWFPFGAFIVGAASYEGSDLAAREKVVLFQHLRGLFGFLSTDD	205
Db	227	APARAFGDPQLPVMWFPFGAFIVGAASYEGSDLAAREKVVLFQHLRGLFGFLSTDD	286
Qy	206	SHARGNWGLLDQAAALRWQENIAARFGDPGNVTLFGQSAGAWSISGLNWSPLASGLFHR	265
Db	287	SHARGNWGLLDQAAALRWQENIAARFGDPGNVTLFGQSAGAWSISGLNWSPLASGLFHR	346
Qy	266	AISQSGTALFRFITNSPLKVAKKVAHLACGNHNSQTILVNCRLALSGTKVMRVSNKXRF	325
Db	347	AISQSGTALFRFITNSPLKVAKKVAHLACGNHNSQTILVNCRLALSGTKVMRVSNKXRF	406
Qy	326	LQINFORDEEIIWNSPVDGVIPDDPLVLLTQKQVSSVYLLGVNNLENNLLPYIM	385
Db	407	LQINFORDEEIIWNSPVDGVIPDDPLVLLTQKQVSSVYLLGVNNLENNLLPYIM	464
Qy	386	KPPLNRQAMRKETITQVLWSTRLLNITKEQVPLVVEEYLDNVNEHDWKLNRNMWDIVQ	445

Db 465 -----NITKEQPLVVEYLDVNEHDWKLNRNMDIVQ 499  
QY 446 DATEVYATLOTAYHRD 462  
Db 500 DATEVYATLOTAYHRE 516  
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; Sequence 254, Application US/09981915A  
; Publication No. US20030054986A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC12  
; CURRENT APPLICATION NUMBER: US/09/981,915A  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 65.1%; Score 2026.5; DB 10; Length 545;
Best Local Similarity 80.3%; Pred. No. 3.6e-185;
Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

; 6 LPSTVLPSSLPAGAGWSNWLCLWSLTLCLMAOTFALCALHTKRPQVVTYKGTLOGKQH 65
; 47 LOSTSTPATTSPSSGFGTGLFGSKPAGTGLTGTNTGALHTKRPQVVTYKGTLOGKQH 106

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QY 66 VGKTPIQVFLGVFPFSRPPLGILRFAPEPEPEPWKGIRDATTYPG----- 110
Db 107 VGKTPIQVFLGVFPFSRPPLGILRFAPEPEPEPWKGIRDATTYPGWSLALSPGWSAVARS 166
QY 111 -----CLQESWQCLASMYVSTRERYKWLRFSDCLYLVNY 145
Db 167 RLTAATSASRVQASLLPQLPLSVMGYRCLQESWQCLASMYVSTRERYKWLRFSDCLYLVNY 226
QY 146 APARAGDPQLPVMWFFPGGATVGAASSYEGSDLAAREKVVLFLOHRLGIFGFLSTDD 205
Db 227 APARAGDPQLPVMWFFPGGATVGAASSYEGSDLAAREKVVLFLOHRLGIFGFLSTDD 286
QY 206 SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTILFGQSAGAMSISGLMMSPLASGLFHR 265
Db 287 SHARGNWGLLDQMAALRWVQENIAAFGGDPGNVTILFGQSAGAMSISGLMMSPLASGLFHR 346
QY 266 AISQSGTALFRIFITSNPLKVAHVLAAGCHNHTQILVNCRLALSGTKVVRVSNKXRF 325
Db 347 AISQSGTALFRIFITSNPLKVAHVLAAGCHNHTQILVNCRLALSGTKVVRVSNKXRF 406
QY 326 LQNFORDPEEIIWMSPVVDGWIPDDPLVLTGKYSVSPYLLGVNVLNLEPNWLLPYIM 385
Db 407 LQNFORDPEEIIWMSPVVDGWIPDDPLVLTGKYSVSPYLLGVNVLNLEPNWLLPYIM 464
QY 386 KFFLNQAVRKETITKMLWSTETLNTITKEQVPLVVEYLDNVNHDWMLRNRMMDIVQ 445
Db 465 -----NITKEQVPLVVEYLDNVNHDWMLRNRMMDIVQ 499
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Db 500 DATEVYATLOTARYHRE 516

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC14
; CURRENT APPLICATION NUMBER: US/09/978,824
; PRIOR FILING DATE: 2001-10-17
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250

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Thu Aug 12 09:48:52 2004

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; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Query Match      65.1%; Score 2026.5; DB 10; Length 545;
Best Local Similarity 80.3%; Pred. No. 3.6e-185;
Matches 399; Conservative 5; Mismatches 26; Indels 67; Gaps 2;

QY      6 LPSTVLPSPPTAGAGWNRWILCSLTLCLMAQTALCALHTKRPQVVTYGTLOGKQMH 65
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47 LGSTSTPATTSAPSGSGFGTGLGSKPATGFTLGGTNTGALHTKRPQVVTYGTLOGKQMH 106
QY      66 VGKTPIQVFLGVFRRPPLGILRFAPPEPPEPWKGIKRDATTYPPG----- 110
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107 VGKTPIQVFLGVFRRPPLGILRFAPPEPPEPWKGIKRDATTYPPGWSLALSPGWSAVARS 166
QY      111 -----CLOESWQQLASMTVSTRERYKWLRFSEDCLYLNYY 145
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167 RLATTSASRVOASLLPQPLSVWGYCLOESWQQLASMTVSTRERYKWLRFSEDCLYLNYY 226
QY      146 APARAPDPQLPVMWPGGAFIVGAASYESGDLAAREKVVLVFLQHLGIFGFLSTDD 205
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347 AISQGTALFRFITSNPLKVAHVLAHLAGCNHNSITLIVNCLRALSGTKWRSVSNKWR 406
QY      326 LQNFQDPEEIIWMSPPVVDGWIIPDDPLVLTQGVSSVPYLLGVANNLEFNWLLPYIM 385
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
407 LQNFQDPEEIIWMSPPVVDGWIIPDDPLVLTQGVSSVPYLLGVANNLEFNWLLPY-- 464
QY      386 KFPENQAMRKETITKMLWSTRLLNITKEQVPLVVEEYLDNVDNHEHDKMLNRNMWDIVQ 445
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
465 -----NITKEQVPLVVEEYLDNVDNHEHDKMLNRNMWDIVQ 499
QY      446 DATFVYATLQTAHYRD 462
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500 DATFVYATLQTAHYRE 516
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Search completed: August 3, 2004, 22:34:11  
Job time : 52 secs

GenCore version 5.1.6  
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QM protein - protein search, using sw model

Run on: August 3, 2004, 22:25:31 ; Search time 21 Seconds

(without alignments)  
2675.041 Million cell updates/sec

Title: US-10-001-227-2

Perfect score: 3112

Sequence: 1 MFSTVLPSTVPSLLPTAGA.....KMAFWMSLYQSQRPEKQRF 584

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR 78:\*\*

2: pir1:\*\*

3: pir2:\*\*

4: pir3:\*\*

5: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1290.5	41.5	557	2 A47162	thiolesterase B (EC 3.1.1.1)
2	1254	40.3	565	2 S10367	carboxylesterase (EC 3.1.1.1)
3	1251	40.2	567	1 A41010	carboxylesterase (EC 3.1.1.1)
4	1239.5	39.8	566	2 S19307	carboxylesterase (EC 3.1.1.1)
5	1205.5	38.7	561	2 JC2447	carboxylesterase (EC 3.1.1.1)
6	1205.5	38.7	562	2 A55281	carboxylesterase (EC 3.1.1.1)
7	1187.5	38.2	561	2 S71597	carboxylesterase (EC 3.1.1.1)
8	1184.5	38.1	561	2 S62788	carboxylesterase (EC 3.1.1.1)
9	1159.5	37.3	549	2 JX0054	carboxylesterase (EC 3.1.1.1)
10	1149	36.9	540	2 A31584	carboxylesterase (EC 3.1.1.1)
11	1141.5	36.7	554	2 A39060	carboxylesterase (EC 3.1.1.1)
12	1133	36.4	539	2 A29323	carboxylesterase (EC 3.1.1.1)
13	1083	34.8	559	1 JC5408	carboxylesterase (EC 3.1.1.1)
14	1060	34.1	561	2 S47855	carboxylesterase (EC 3.1.1.1)
15	1034	33.2	554	1 S34607	carboxylesterase (EC 3.1.1.1)
16	993	31.9	532	2 A34329	60K esterase (EC 3.1.1.1)
17	787	25.3	614	2 A39256	acetylcholinesterase (EC 3.1.1.1)
18	761.5	24.5	614	2 JH0314	acetylcholinesterase (EC 3.1.1.1)
19	751.5	24.1	614	2 JH0811	acetylcholinesterase (EC 3.1.1.1)
20	741	23.8	584	2 S48724	acetylcholinesterase (EC 3.1.1.1)
21	740.5	23.8	583	2 S10712	acetylcholinesterase (EC 3.1.1.1)
22	727	23.4	612	2 A34967	sterol esterase (EC 3.1.1.1)
23	726	23.3	599	2 A57701	sterol esterase (EC 3.1.1.1)
24	725.5	23.3	596	1 ACRYE	acetylcholinesterase (EC 3.1.1.1)
25	722	23.2	597	2 A33658	sterol esterase (EC 3.1.1.1)
26	713.5	22.9	599	1 A38868	acetylcholinesterase (EC 3.1.1.1)
27	712.5	22.9	602	1 ACHU	acetylcholinesterase (EC 3.1.1.1)
28	702	22.6	745	2 S13586	triacylglycerol 11
29	691	22.2	603	2 S70849	cholinesterase (EC 3.1.1.1)

acetylcholinesterase (EC 3.1.1.1)  
cholinesterase (EC 3.1.1.1)  
para-nitrobenzyl e  
acetylcholinesterase (EC 3.1.1.1)  
triacylglycerol 11  
triacylglycerol 11  
carboxylesterase (EC 3.1.1.1)  
acetylcholinesterase (EC 3.1.1.1)  
acetylcholinesterase (EC 3.1.1.1)  
protein 128C12.4b  
hypothetical prote  
carboxylesterase (EC 3.1.1.1)  
acetylcholinesterase (EC 3.1.1.1)  
acetylcholinesterase (EC 3.1.1.1)  
probable esterase (EC 3.1.1.1)

## ALIGNMENTS

### RESULT 1

A47162

thiolesterase B (EC 3.1.1.1) precursor - mallard

C:Species: Anas platyrhynchos (mallard)

C>Date: 05-May-1995 #sequence\_revision 05-May-1995 #text\_change 18-Jun-1999

C:Accession: A47162

R:Hwang, C.S.; Kolatukudy, P.E.

J. Biol. Chem. 268, 14278-14284, 1993

A:Title: Molecular cloning and sequencing of thioesterase B cDNA and stimulation of exp

A:Reference number: A47162; NID:93300823; PMID:8314791

A:Accession: A47162

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-557 <HWA>

A:Cross-references: GB:L05493; NID:G213100; PIDN:AAA49223.1; PID:G213101

A:Superfamily: cholinesterase; cholinesterase homology

C:Keywords: hydrolase

F:56-545/Domain: cholinesterase homology <CH>

Query Match 41.5%; Score 1290.5; DB 2; Length 557;  
Best Local Similarity 46.0%; Pred. No. 1.4e-96;  
Matches 260; Conservative 106; Mismatches 172; Indels 27; Gaps 11;

QY 27 ILCSLTCLMAQTALGALHTKRPQVTKYGTLOGKQHV--GKTPTQVFLGVFSPPL 84  
Db 8 LLSLTILTAGITAVTQG-KAEQPEVNTYGVYQVKNAAERSVNVFLGLPFAKPPV 66  
QY 85 GILFAPPEPEPKGIRDTATTPGCLQES-WQLASMYVSTRERYKWLRFSDCLYN 143  
Db 67 GLRFSEQPEPKGVRDAASYPMLQDVKLOYSDAITNKEKVRLOISDCLYN 126  
QY 144 VYAPARPGDPQLPVMVFPQAFIVGAASYESGDLAAREKVVVLFQHLRIGFGLST 203  
Db 127 VYTPVSTEEQKLPVFMVHGGGLVSGAASVYDGSALAAFDNVVVTIYRLGIAGVPST 186  
QY 204 DSHARGNGWGLDQWALRWYQENIAFGDPGNVTLFGOSAGAMSISGLMMSPLASGLF 263  
Db 187 GDKARGNGWGLDQWALRWYQENIAFGDPGNVTLFGOSAGAMSISGLMMSPLASGLF 246  
QY 264 HRAISQSGTALFRIFITSNPLKVAKVAHLACGNHNSITQILVNCRLRSLGTVKVRVSNKM 323  
Db 247 HKAISESGTAV-RILFTQPEEQARIAAAGCEKSSAALVECLREKTEAEHQITLKM 305  
QY 324 RFLQNFORDPEEIIWMSVVDGVIPDDPLVLLTQGVSSVYLLGVNNLEFNWLLPY 383  
Db 306 -----PPMFI---SASLDGVFPFKSPRLSEKVINAVPYIIGVNNCFEGWILPR 352  
QY 384 IMKPELNFQAMRKETITKMLWSTRL--LNTKQVPLAVVEYLDNVNEHDKMLNRNM 441  
Db 353 MKKPEFTEGLEKDVQVQLSTLALSKFAPSIVDLVYNEYI-GVAENR-AQVRDGLL 410  
QY 442 DIVQDATFVYATLOTAYVHRDAGLPVLYIEFEHH---ARGIIVKPRTDGADHGDMEYPLF 498





R:Zschunke, F.; Salmassi, A.; Kreipe, H.; Buck, F.; Parwaresch, M.R.; Radzun, H.J.  
 Blood 78, 506-512, 1991  
 A:Title: cDNA cloning and characterization of human monocyte/macrophage serine esterase-1  
 A:Reference number: A49816; MUID:91300111; PMID:2070086  
 A:Accession: A49816  
 A:Molecule type: mRNA  
 A:Residues: 'G', 65-185, 'G', 187-361, 363-567 <ZSC>  
 A:Cross-references: GB:X52973; NID:G36421; PIDN:CAA37147.1; PID:g1335304  
 R:Ridgley, P.W.; Richards, L.J.; Bowles, M.R.; Pond, S.M.  
 Gene 108, 289-292, 1991  
 A:Title: Cloning and analysis of a cDNA encoding a human liver carboxylesterase.  
 A:Reference number: P80280; MUID:92084150; PMID:1748313  
 A:Accession: P80280  
 A:Molecule type: mRNA  
 A:Residues: 114, 'H', 116-280, 'A', 282-300, 'IGNSYLTYRETREST', 318-336, 'R', 338-382, 'GSP', 384-400  
 A:Cross-references: GB:M65261; NID:G187028; PIDN:AAA83932.1; PID:g187029  
 A:Experimental source: liver  
 A:Note: differences between this sequence and other reports appear to be due to frameshift  
 R:Koetz, D.L.; McBride, O.W.; Gonzalez, F.J.  
 Biochemistry 32, 11606-11617, 1993  
 A:Title: Glycosylation-dependent activity of baculovirus-expressed human liver carboxylesterase  
 A:Reference number: A48809; MUID:94032283; PMID:8218228  
 A:Accession: I61085  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-55, 'G', 57-361, 363-535, 'G', 537-567 <KRO1>  
 A:Cross-references: GB:L07765; NID:G180949; PIDN:AAA35711.1; PID:g180950  
 A:Accession: A48809  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-17, 'A', 18-55, 'G', 57-535, 'G', 537-567 <KRO2>  
 A:Cross-references: GB:L07764; NID:G180947; PIDN:AAA16036.1; PID:g180948  
 C:Genetics:  
 A:Gene: GDB:CES1; HMSC  
 A:Cross-references: GDB:128044; OMIM:114835  
 A:Map position: 16q13-16q22.1  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; liver  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-145/Domain: propeptide #status predicted <PRO>  
 F:50-553/Domain: cholinesterase homology <CHE>  
 F:146-567/Product: carboxylesterase #status experimental <MAT>  
 F:564-567/Region: endoplasmic reticulum retention signal #status atypical  
 F:221,468/Active site: Ser, His #status predicted

Query Match 40.2%; Score 1251; DB 1; Length 567;  
 Best Local Similarity 44.2%; Pred. No. 2.3e-33;  
 Matches 250; Conservative 111; Mismatches 192; Indels 12; Gaps 9;  
 QY 26 WILCWSLTLCLMAQTALGALHTKRPQVV-TKYGTLOK--QMHVGKTPICVFLGVFPSP 82  
 DB 2 WLRATILA-TLSAANG--HPSPPPVVDVHCKVLGKFLVLEGGFAQPAIFLGIPIPAK 58  
 QY 83 PLGILRAPPEPPKGIKIRDAITYPPGCLQE-SWGLQASMYVSTRERYKWLRFSDCLY 141  
 DB 59 PLGLRFTPPQAPSPFVKNATSYPPMCTQDPKAGLLSELFTNKENIPLKLSBCLY 118  
 QY 142 LNVYAPARPGDPOLPVMVWFGGATVGAASVEGSDLAAREKVVLFQHLRIGFGL 201  
 DB 119 LNIYTPADLTKKRLPVMWVHGGGLMVGASTYDGLAAAHENVVVTIQRLLGWGF 178  
 QY 202 STDDSHARGNWGLLDQMAALRWYQENIAAPGGDPGNVTIFGOSAGAMISGLMMSPLASG 261  
 DB 179 STGDESRGNWGLDQVAALRWYQENIAAPGGDPGNVTIFGOSAGAMISGLMMSPLAK 238  
 QY 262 LFRATISQSTALFRFLFITSNPLK-VAKKVAHLACGNHNSSTOLLVNCIRALSGTKMVRVS 320  
 DB 239 LFRATISESVALTSLVKKGVDPKLAEQIAITAGCKTTISAVVHCLRQKTEBELLETT 298  
 QY 321 NKMRFLQNFQRPDEEIIWMSPVVDGVPDPDDLVLTAQGVSSVYLLGVNLEFNWL 380  
 DB 299 LKMKFLSLDLDQGPRESQPLGLTVIDGMLLLKTFEELQAEENFHTVYVVGINKQEFGL 358

QY 381 LP-YIMKPEPLNRQAMRKETITKMLASTRTLLNITKEQVPLVVEEYLDNVNHEHDKMLNR 439  
 DB 359 IPWQLMSYPLSGQDDQKATMSLLWKSPLVCIKALPEATEKYLGGTD--DTVKKKDL 416  
 QY 440 MMDIVODATFVYATLQTAHYHRDAGLPVYLXFEHH-ARGIIVKPTDGAHDGDMYFLF 498  
 DB 417 FLDLIADVMFGVPSVIVARNHRDAGAPTVMYEFQVRPSFSSDMKPKTVIGDGHDLFSVF 476  
 QY 499 GGPEATGLSMGKEKALSQMKMYWANEARTGNPNNGNLPCWPRYKNDKYLQDLDTTRVG 558  
 DB 477 GAFFLKEGASEEIEILSKVMKFWANFARNGPNNGEGLPFWPEYKQEGYLQIGANTQAA 536  
 QY 559 MKLKEKMAFMMSLYQSQRPEKQ 583  
 DB 537 QKLKDEKAVAFWNLFAKKAVERPPQ 561  
 RESULT 4  
 S19307  
 C:carboxylesterase (EC 3.1.1.1) precursor - pig  
 N:Alternate names: proline-beta-naphthylamidase  
 C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 18-Jun-1999  
 C:Accession: S19307; S23607  
 R:Watsushima, M.; Inoue, H.; Ichinose, M.; Teukada, S.; Miki, K.; Kurokawa, K.; Takahashi  
 FEBS Lett. 293, 37-41, 1991  
 A:Title: The nucleotide and deduced amino acid sequences of porcine liver proline-beta-  
 A:Reference number: S19307; MUID:92070571; PMID:1959668  
 A:Accession: S19307  
 A:Molecule type: mRNA  
 A:Residues: 1-566 <MAT1>  
 A:Cross-references: EMBL:X63323; NID:G1930; PIDN:CAA44929.1; PID:g1931  
 A:Molecule type: protein  
 A:Residues: 19-40 <MAT2>  
 A:Note: 28-Lys and 33-Leu were also found  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; homotrimer  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-566/Product: carboxylesterase #status experimental  
 F:51-552/Domain: cholinesterase homology <CHE>  
 F:80/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:222,467/Active site: Ser, His #status predicted

Query Match 39.8%; Score 1239.5; DB 2; Length 566;  
 Best Local Similarity 44.2%; Pred. No. 2e-92;  
 Matches 248; Conservative 110; Mismatches 192; Indels 11; Gaps 7;  
 QY 26 WILCWSLTLCLMAQTALGALHTKRPQVV-TKYGTLOKQMHVG--KTIQVFLGVFPSP 82  
 DB 2 WLL--PLVLTSLASATWAGOPAPFPVDTAQRVLKYSLEGLAQDPAVFLGVFPAPK 59  
 QY 83 PLGILRAPPEPPKGIKIRDAITYPPGCLQESWGQ--LASMVYSTRERYKWLRFSDCL 140  
 DB 60 PLGLRFTPPQAPSPFVKNATSYPPMCCQDPVVEQWTSDFLTNGKRLT-LEFSDCL 118  
 QY 141 LNVYAPARPGDPOLPVMVWFGGATVGAASVEGSDLAAREKVVLFQHLRIGFGL 200  
 DB 119 LNIYTPADLTKKRLPVMWVHGGGLVGGAPMDGVVLAHENVVVAIQRLGWGF 178  
 QY 201 STDDSHARGNWGLLDQMAALRWYQENIAAPGGDPGNVTIFGOSAGAMISGLMMSPLAS 260  
 DB 179 STGDESRGNWGLDQVAALRWYQENIAAPGGDPGNVTIFGOSAGAMISGLMMSPLAK 238  
 QY 261 LFRATISQSTALFRFLFITSNPLKVAKKVAHLACGNHNSSTOLLVNCIRALSGTKMVRVS 320  
 DB 239 LFRATISESVALTSLVKKGVDPKLAEQIAITAGCKTTTSAVFHCLRQKSEDELLDT 298  
 QY 321 NKMRFLQNFQRPDEEIIWMSPVVDGVPDPDDLVLTAQGVSSVYLLGVNLEFNWL 380  
 DB 299 LKMKFLSLDLDQGPRESQPLGLTVIDGMLLLKTFEELQAEENFHTVYVVGINKQEFGL 358  
 QY 381 LPYIMKPEPLNRQAMRKETITKMLASTRTLLNITKEQVPLVVEEYLDNVNHEHDKMLNR 440

Db 359 LPTMGFPSEGLDKQKATSLWKSYPANIPDELTPVATDKYLGCTDDPKV--KDLF 416  
 Qy 441 MDIVQDATFYATLQAHYHRDAGLVLYLYFEHH--ARGIIIVKPRDTGADHDEMYFLFG 499  
 Db 417 LDLMGDVFGVPSVTVARQHDAGATYMFQYRPSFSSDKKPKTVIGDHGDEIFSVFG 476  
 Qy 500 GPATGLSMGKEKALSQMKYKWNANFARTGNPDGMLPCWPRYNKDEKYLQDFTTRVGM 559  
 Db 477 FPLKGDAPDEEVSLSKTVKFWANFARNSPNEGELPHMPYDQBEGLQIGVNTQAAK 536  
 Qy 560 KLEKEMAFWMSLYQSORPEK 580  
 Db 537 RLKGEVAFWNDLLSKEAKK 557

## RESULT 5

JC2447  
 carboxylesterase (EC 3.1.1.1) ES-3 precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 29-Mar-1995 #sequence\_revision: 26-May-1995 #text\_change 18-Jun-1999  
 C:Accession: JC2447; S23462  
 R:Robbi, M.; Beaufay, H.  
 Biochem. Biophys. Res. Commun. 203, 1404-1411, 1994  
 A:Title: Cloning and sequencing of rat liver carboxylesterase ES-3 (EGASYN).  
 A:Reference number: JC2447; MUID:95032008; PMID:7945287  
 A:Accession: JC2447  
 A:Molecule type: mRNA  
 A:Residues: 1-561 <ROB>  
 A:Cross-references: GB:X81395; NID:G550146; PIDN:CAA57158.1; PID:G550147  
 A:Experimental source: liver  
 R:Medda, S.; Proia, R.L.  
 Eur. J. Biochem. 206, 801-806, 1992  
 A:Title: The carboxylesterase family exhibits C-terminal sequence diversity reflecting  
 A:Reference number: S23460; MUID:92299008; PMID:1606962  
 A:Accession: S23462  
 A:Status: preliminary; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 503-554, 'R', 556-561 <MED>  
 A:Cross-references: EMBL:X65295; NID:G57557; PIDN:CAA46390.1; PID:G57558  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-561/Product: carboxylesterase ES-3 #status predicted <SIG>  
 F:50-551/Domain: cholinesterase homology <CHE>  
 F:79,107,489/Binding site: carbohydrate (Asn)  
 F:221,466/Active site: Ser, His #status predicted

Query Match 38.7%; Score 1205.5; DB 2; Length 561;  
 Best Local Similarity 43.3%; Pred. No. 1.1e-89;  
 Matches 238; Conservative 114; Mismatches 191; Indels 7; Gaps 6;  
 Qy 28 LC-MSLTLCLMAQTALGALHTKRPQVVTYKGTLOGKQMHV-GKT-PIQVFLGVFSPRPPL 84  
 Db 1 MCLVALILVFLAFTAGGHSSLPVDTLQKVLGKVSLEGFTQPVAVFLGVFAKPL 60  
 Qy 85 GILRFAPPEPEPKGRDATTYPGCLQES-WGOLASMYVSTRYKMLRSEDCLYLN 143  
 Db 61 GSLRFAPQPAEPWSFKNTSYPPMCSQDPVAGQIVNDLLTNWENISLQFSEDCLYLN 120  
 Qy 144 VYAPARAPGDPOLPVMVWVFGAFIVGAASVSGSDLAAREKVVFLQRLHGFGLST 203  
 Db 121 IYTPADLTKRDLRPLFWMIHGGGLVLGASTYDGLALSTHENVVVVIQYRLGIWGFST 180  
 Qy 204 DDSHARGNWGLLDQMAALRWQENIAAFPGDPGNVTLFGQSAGMSISGLMWSPGLF 263  
 Db 181 GDEHSRGNWGLDQVAALHWQDNIIDNFGDPGSGVTIFGESAGGESVSLVLSPLAKLUF 240  
 Qy 264 HRAISQSTALFRFLFITSNPLKVAKVLAHLAGCNHNSTQILVNCRLALSGTKVMRSNM 323  
 Db 241 HKALISGSVALTAGLVKNTPLAEKIAVSGCKSTISASWVHCLQRKTEEBELTTLK 300  
 Qy 324 RFLQNFORDPEEIIWSNPSVVDGVIPDDPLVLLTOGKVSVPYLLGVNNLEFNPWLPY 393

Db 301 NLFSLDLHGDSRQSPVPVTLVDGVVLPKMPPEILAEKDFNTVPYIVGINKOEFGWILFT 360  
 Qy 384 IMKFPPLNRQMRKETITTKMLWSTRTLLNITKEQVPLVVEEYLDNVNHEHDKMLRNHMDI 443  
 Db 361 MMNYPSPDKLDPMATATSLKSSFLNUPPEEAPVAVSEKYLRLHTDDPDRN--KDQLLSL 418  
 Qy 444 VQDATFYATLQAHYHRDAGLVLYLYFEHH--ARGIIIVKPRDTGADHDEMYFLFGPFP 502  
 Db 419 IGDVIFGVPSTVYSGHRDAGARTYMFQYRPSFSSKMKFSTVVGHDGDEIVSVFGAP 478  
 Qy 503 ATGLSMGKEKALSQMKYKWNANFARTGNPDGMLPCWPRYNKDEKYLQDFTTRVGMKLC 562  
 Db 479 LRGGTSKEEINLSKMMKFWANFARNSPNEGOLPHMPYDQBEGLQIGATTQQAOKLR 538  
 Qy 563 EKKMAFWMSL 572  
 Db 539 EXEVAFWSEL 548

## RESULT 6

A55281  
 carboxylesterase (EC 3.1.1.1) egasyn - mouse  
 N:Altername names: beta-glucuronidase endoplasmic reticulum-targeting protein; esterase-  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Feb-1995 #sequence\_revision 10-Feb-1995 #text\_change 18-Jun-1999  
 C:Accession: A55281  
 R:Ovnic, M.; Swank, R.T.; Fletcher, C.; Zhen, L.; Novak, E.K.; Baumann, H.; Heintz, N.;  
 Genomics 11, 956-967, 1991  
 A:Title: Characterization and functional expression of a cDNA encoding egasyn (esterase-  
 A:Reference number: A55281; MUID:92147141; PMID:1783403  
 A:Accession: A55281  
 A:Status: preliminary  
 A:Molecule type: mRNA; protein  
 A:Residues: 1-562 <OVN>  
 A:Cross-references: GB:S80191; NID:G244727; PIDN:AAB21335.1; PID:G244728  
 A:Note: sequence extracted from NCBI backbone (NCBIN:80191, NCBI:P:80194)  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum  
 F:51-552/Domain: cholinesterase homology <CHE>  
 F:222,467/Active site: Ser, His #status predicted

Query Match 38.7%; Score 1205.5; DB 2; Length 562;  
 Best Local Similarity 42.4%; Pred. No. 1.1e-89;  
 Matches 241; Conservative 119; Mismatches 188; Indels 21; Gaps 9;  
 Qy 28 LCWS-LTLCLMAQTALGALHTKRPQVVTYKGTLOGKQMHV-----TPIQVFLGV 78  
 Db 1 MCLVALILVSLAFTAGAGHPSSPPMV---DTVQGVKYL--GKVISLEGFTQPVAVFLGV 55  
 Qy 79 FSRPLGLTRFAPPEPEPKGRDATTYPGCLQES-WGOLASMYVSTRYKMLRSEDCLYLN 137  
 Db 56 FAKPLGSLRFPAPQPAEPWSFKNTSYPPMCSQDPVAGQIVNDLLTNKKEIPLQFSE 115  
 Qy 138 DCLYLVYAPARAPGDPOLPVMVWVFGAFIVGAASVSGSDLAAREKVVFLQRLHGI 197  
 Db 116 DCLYLVNITPADLTKRDLRPLFWMIHGGGLVLGASTYDGLVLTSHENVVVVIQYRLGI 175  
 Qy 198 PGFLSTDDSHARGNWGLLDQMAALRWQENIAAFPGDPGNVTLFGQSAGMSISGLMWSP 257  
 Db 176 WGFSTGDEHSRGNWGLDQVAALHWQDNIIDNFGDPGSGVTIFGESAGGESVSLVLS 235  
 Qy 258 LASGLFHRAISQSTALFRFLFITSNPLKVAKVLAHLAGCNHNSTQILVNCRLALSGTKVM 317  
 Db 236 LAKNLFQRAISGSVALTAGLVKNTPLAEKIAVSGCKNTTSAAMVHCLQRKTEEBEL 295  
 Qy 318 RVSNKORFLQNFORDPEEIIWSNPSVVDGVIPDDPLVLLTOGKVSVPYLLGVNNLEF 377  
 Db 296 GTTLKLNLFKLDLHGDSRQSPHPVPTVLDGVLLPMPPEEILAEKNTVYIVGINKQEP 355  
 Qy 378 NWLLPYIMKFPPLNRQMRKETITTKMLWSTRTLLNITKEQVPLVVEEYLDNVNHEHDK-ML 436  
 Db 356 GWILPTMWNYPSPDKLDPMATATSLKSSFLNUPPEEILAEKNTVYIVGINKQEP 412

Qy	437	RNRMMDIVODATFVYATLCTAHYHRDAGLPVLYEFEBH-ARGIIVPRTDGDAGHGDEMY	495
Dd	413	KDQLLELIGDVGVPFVSIVSRGHRDAGAPTYMEFYQSPFSSEMXPDTWVGCHGEIY	472
Qy	496	FLFGGPFATGLSGKGEKALSLQMKMYWANFARTGNPNPNDGILPCWPRYNKCEKYLQLDFTT	555
Dd	473	SVFGAPILSGTSEEBEINLSKMKMFANFARNGNPNPQGLPFWPEYDQKEGYLQIGATT	532
Qy	556	RVGMKULKEKMAFWMSLY-QSORPEKQKQ	583
Dd	533	QQAQKLKEKEVAFWTELLAKQLPTEHTE	561

RESULT 7  
S71597  
carboxylesterase (EC 3.1.1.1) precursor, liver - rat  
N:Alternate names: hydrolase C  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 13-Sep-1998  
C:Accession: S71597  
R:Yan, B.; Yang, D.; Parkinson, A.  
Arch. Biochem. Biophys. 317, 222-234, 1995  
A:Title: Cloning and expression of hydrolase C, a member of the rat carboxylesterase family  
A:Reference number: S71597; MUID:95177656; PMID:7872788  
A:Accession: S71597  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-561 <YAN>  
A:Experimental source: liver; endoplasmic reticulum  
C:Function:  
A:Description: catalyzes conversion of carboxylic ester to alcohol and carboxylic anion  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver  
F:1-18/Domain: signal sequence #status predicted <SIG>  
F:19-561/Product: carboxylesterase #status predicted <MAN>  
F:50-551/Domain: cholinesterase homology <CHE>  
F:558-561/Region: endoplasmic reticulum retention signal  
F:79,301/Binding site: carbohydriate (Asn) (covalent) #status predicted  
F:221,466/Active site: Ser, His #status predicted

Query Match	38.2‡	Score 1187.5	DB 2	Length 561
Best Local Similarity	41.1‡	Pred. No. 3.2e-88		
Matches 230	Conservative 123	Mismatches 196	Indels 11	Gaps 5

Qy	24	MZWILCWSLTLCLMA--QTALGALHTRKPQVWTKYGTLOGQMHVGKTPIQVFLGVFFSR	81
Db	3	L\$SLFLVSLATCWCNGN\$SP\$PVVD\$TK\$KVLGKYASLEGTQ\$VA-----VFLGVFFAK	57
Qy	82	PBLGTLIRAPPEPPPMKIGIRCATYTPGCLQESW-QOLASMYVSTREYKMWLRSEDCI	140
Db	58	PLGSLRFAPOPAEPFW\$VKN\$T\$YTPMCSQD\$ATKQ\$RVNDL\$TLNRKEVHLQ\$FSEDCI	117
Qy	141	YLN\$VAPARA\$PGDPOLP\$VWVW\$PFGA\$FTVGA\$S\$YEG\$DLAAREK\$VVL\$VFLQ\$RLIG\$IFQ	200
Db	118	YLN\$YITPAD\$FTK\$D\$EMP\$VWVW\$HGG\$LTQ\$G\$ASTYD\$GVLS\$AVEN\$VWVW\$VAI\$QY\$RLG\$W\$F	177
Qy	201	L\$TDSHARGN\$GLLDQ\$AALRW\$QEN\$IAAP\$GDP\$GNV\$TLFG\$SAGAM\$SIGL\$M\$PLAS	260
Db	178	F\$TGDEH\$RGNGW\$HLDQ\$VAA\$LHWYQD\$NIAN\$FGDP\$G\$V\$TIF\$G\$AG\$F\$SV\$V\$L\$V\$PL\$K	237
Qy	261	GLF\$HRAI\$QS\$G\$TAL\$FRL\$IT\$N\$PLK\$VAK\$YAH\$LAGN\$HN\$TQ\$ILNCLRAL\$S\$TK\$V\$W\$V\$S	320
Db	238	NIY\$HRAI\$B\$S\$GV\$VLTQ\$FTK\$D\$V\$P\$AAQ\$AD\$MAG\$CK\$T\$T\$SA\$IV\$HCL\$Q\$K\$T\$EE\$LE\$T\$M	297
Qy	321	N\$X\$RFLQ\$LN\$FQ\$RDP\$BEI\$W\$MS\$PV\$VD\$GV\$IP\$DD\$PL\$V\$LL\$TQ\$K\$V\$SV\$PY\$LL\$G\$V\$N\$N\$F\$E\$W\$L	380
Db	298	EX\$N\$LL\$K\$S\$Q\$R\$D\$T\$K\$E\$S\$YH\$F\$L\$T\$V\$D\$D\$V\$LP\$K\$P\$K\$E\$LA\$E\$K\$N\$T\$N\$T\$PY\$IV\$G\$INK\$Q\$C\$G\$W\$	357
Qy	381	L\$Y\$IMK\$F\$PL\$N\$Q\$M\$K\$E\$T\$IT\$K\$M\$L\$S\$TR\$T\$FL\$N\$IT\$K\$E\$Q\$V\$L\$V\$B\$Y\$E\$LV\$D\$N\$V\$H\$D\$W\$K\$M\$L\$R\$N\$R\$M	440
Db	358	L\$P\$TM\$R\$F\$V\$P\$D\$VK\$D\$K\$Q\$AI\$ML\$B\$K\$F\$AS\$IV\$G\$IED\$IP\$V\$AI\$E\$K\$Y--R\$K\$G\$D\$D\$P\$K\$IR\$D\$I	415

Qy	441	MDIVQDAIVFVATLQTAHYHEDAGLPVLYFEFHH-ARGIIIVXPRTDGDAGDEMVFELG	499
Db	416	LAFIGBVLFCIPFVMSVSRDDAGAPTYIYQYFSPQSPQKVGVGDHADVVSFVG	475
Qy	500	GFATGLSGKGEKALSLQMKYKWNANFARTGNPDGNLPCWPRYKNKBEKYLQLDFTTRVGM	559
Db	476	APILRDGASBEEIKLSKVMKMFANFARNGNPNARGLPHWPQDYQKEEYLQIGATTQQSQ	535
Qy	560	KLUKEKKMAFMSLYQSQRPE	579
Db	536	RLKABEAVFMTOLLAKRQPO	555

## RESULT 8

carboxylesterase (EC 3.1.1.1) ES-4 precursor, liver - rat

S62788

N:Alternate names: hydrolase B

C:Species: Rattus norvegicus (Norway rat)

C:Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 18-Jun-1999

C:Accession: S62788; S51203; A55304; S49257

R:Robbi, M.; van Schaftingen, E.; Beaufay, H.

Biochem. J. 313, 821-826, 1996

A:Title: Cloning and sequencing of rat liver carboxylesterase ES-4 (microsomal palmitoyl

A:Reference number: S62788; MUID:96150723; PMID:8611161

A:Accession: S62788

A:Molecule type: mRNA

A:Residues: 1-561 <ROB>

A:Cross-references: EMBL:X81825; NID:G550417; PIDN:CAA57419.1; PID:G550418

A:Experimental source: liver

R:Morgan, E.W.; Yan, B.; Greenway, D.; Petersen, D.R.; Parkinson, A.

Arch. Biochem. Biophys. 315, 495-512, 1994

A:Title: Purification and characterization of two rat liver microsomal carboxylesterase

A:Reference number: S51202; MUID:95077430; PMID:7986098

A:Accession: S51203

A:Molecule type: protein

A:Residues: 19-48 <MOR>

A:Experimental source: liver

R:Yan, B.; Yang, D.; Brady, M.; Parkinson, A.

J. Biol. Chem. 269, 29688-29696, 1994

A:Title: Rat kidney carboxylesterase. Cloning, sequencing, cellular localization, and r

A:Reference number: A55304; MUID:95050819; PMID:7961958

A:Accession: A55304

A:Molecule type: mRNA

A:Residues: 1-6, 'F', 8-59, 'P', 61-212, 'A', 214-252, 'T', 254-309, 'IT', 312-341, 'N', 343-424, 'F',

A:Cross-references: GB:U10697; NID:G562007

A:Note: the sequence in GenBank entry RNU10697, release 107, (PID:G562008) has the codon

R:Robbi, M.; Beaufay, H.

Submitted to the EMBL Data Library, September 1994

A:Reference number: S49257

A;Cross-references: EMBL:X81825; NID:g550417; PIDN:CAA57419.1; PID:g550418

C: function:  
 A: description: catalyzes conversion of carboxylic ester to alcohol and carboxylic anion  
 C: superfamily: cholinesterase; cholinesterase homology  
 C: keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein; liver  
 F: 1-18/Domain: signal sequence #status predicted <SIG>  
 F: 19-561/Product: carboxylesterase ES-4 #status experimental <VAT>  
 F: 50-551/Domain: cholinesterase homology <CHE>  
 F: 221-466/Active site: Ser, His #status predicted  
 F: 301/Binding site: carbonylrate (Asn) (covalent) #status predicted

Query Match	38.1%;	Score 1184.5;	DB 2;	Length 561;
Best Local Similarity	41.7%;	Pred. No. 5.6e-88;		

[illegible]

Db 58 PPLGSLRFAFPQPAEPWFSVKNVTTPMCSQDAAGQRMNDLLTNREKIHLEFSEDCL 117  
 Qy 141 YLNVYAPARAGDPQPLPVWFWFGGAFIVGAASSYEGSDLAAREKVVVFLQHRIGIFG 200  
 Db 118 YLNIYTPADFTKNSRLPVMVWIHGGVTLGGASTYDGRVLSAYENVVVAIYQRLIGWGF 177  
 Qy 201 LSTDDSHARGNWGLLDMAALRWQENIAAFGDPGNVTLFGOSAGAMSISGLMSPLAS 260  
 Db 178 PSTGDEHSRGNWGLDVAALHVVQDNIAFGDPGSGVTFGESAGGFSVSLVLSPLTK 237  
 Qy 261 GLPHRAISQSGTALFRLFTITSNPLKVAKVLAHAGNHNSTOILVNCRLALSGLTKMRVS 320  
 Db 238 NLFHRAISESGVFLPGLITKDVRAAKQIADWAGCETTTSATIVCHLRQKTEELLEM 297  
 Qy 321 NKVRFLQNFORDPEEIIWMSFPVGVWIPDDPLVLTQGVKSSVPYLLGVNNLEFNWL 380  
 Db 298 KQNLILKSSQRDNKESYHFLSTVDNVVLPKDPKILAEKPNVTVPYIVGINKQECGWL 357  
 Qy 381 LPYIMKF-PNLRQAMRKETITKMLSTRLLNTITKEQVPLVVEEYLDNVNEHDKWMLNR 439  
 Db 358 LPTWGFVPADVELDKQWAIIT-LLEKFAISLYGIPEDIIPVAIEKY--RKGSDSIRKIDG 414  
 Qy 440 MMDIVQDATFYATLQTAHYHRDAGLPVLYEPEHH-ARGIIIVKPRTDGADHDEMVFLLF 498  
 Db 415 ILAFIGDVSFSPVMSVRDHRDAGAPTYMYEYQYPSFSSPPQPKHVVGCDHADDLYVF 474  
 Qy 499 GGPFPATGLSMGKKEKALSQMKWYANFARTGNPDGNLPCWPRYNKDEKYLQDFTTRVG 558  
 Db 475 GAPTLDGASBEEIKLSKWKWFWANFARNGNPNRGLPHWPQYDQKEEVLQIGATTQOS 534  
 Qy 559 MKLKEKMAFWMSLYQSORPE 579  
 Db 535 QRLKAEVAFWTLAKRQPO 555

RESULT 9  
 JX0054  
 Carboxylesterase (EC 3.1.1.1) El precursor, minor form - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 21-Aug-1998  
 C:Accession: JX0054  
 R: Takagi, Y.; Morohashi, K.; Kawabata, S.; Go, M.; Omura, T.  
 J. Biochem. 104, 801-806, 1988  
 A:Title: Molecular cloning and nucleotide sequence of cDNA of microsomal carboxylesterase  
 A:Reference number: JX0054; MUID:89174514; PMID:3235453  
 A:Accession: JX0054  
 A:Molecule type: mRNA  
 A:Residues: 1-549 (TAK)  
 A:Experimental source: liver  
 A:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein; microsome  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-549/Product: carboxylesterase El #status predicted <MAT>  
 F:50-538/Domain: cholinesterase homology <CHE>  
 F:79,274,302,375,476/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:221,453/Active site: Ser, His #status predicted

Query Match 37.3%; Score 1159.5; DB 2; Length 549;  
 Best Local Similarity 42.6%; Pred. No. 5.8e-06;  
 Matches 240; Conservative 104; Mismatches 192; Indels 27; Gaps 9;

Qy 26 WI--LCW-SUTLCIM--AQTALGALHTKRPQVWTKYGTLOGKQHVGTPIQVFLGVPS 80  
 Db 2 WLCLVWASLAVCPWCHPSSPPVDTTKGVLGVLSLEGFTQ-----PVAVFLGVPA 56  
 Qy 81 RPLGIILRPAPPPEPPKIRADATTPPCLOES--WGQLASMYVSTRERYKWLRFSEDC 139  
 Db 57 KPPLGSLRFAFPPEPWFSPVKNVTTPMCSQDGVVGGKLLDMLSTGKESIPLEFSEDC 116  
 Qy 140 YLNVYAPARAGDPQPLPVWFWFGGAFIVGAASSYEGSDLAAREKVVVFLQHRIGIFG 199  
 Db 117 YLNIYSPADLTNKSRLPVMVWIHGGVTLGGASTYDGRVLSAYENVVVAIYQRLIGW 176

Qy 200 FLSTDDSHARGNWGLLDMAALRWQENIAAFGDPGNVTLFGOSAGAMSISGLMSPLAS 259  
 Db 177 LFTSGDEHSRGNWGLDVAALHVVQDNIAFGDPGSGVTFGESAGGFSVSLVLSPLA 236  
 Qy 260 SGLPHRAISQSGTALFRLFTITSNPLKVAKVLAHAGNHNSTOILVNCRLALSGLTKMRV 319  
 Db 237 KNLFHRAISESGVFLPGLITKDVRAAKQIADWAGCETTTSATIVCHLRQKTEELLEM 297  
 Qy 320 NKVRFLQNFORDPEEIIWMSFPVGVWIPDDPLVLTQGVKSSVPYLLGVNNLEFNWL 379  
 Db 288 KTEAELELTVKLDNT---SMSTVIDGVLPKTPBEILTEKSFNTVPYIVGINKQECGWL 343  
 Qy 380 LLPYIMKFPNLRQAMRKETITKMLSTRLLNTITKEQVPLVVEEYLDNVNEHDKWMLNR 439  
 Db 344 IIPTMWGNLLSEGMNEKMASSFLKRFSPNLNISESVIPAIIEKYLRTGDDPAK--KEL 401  
 Qy 440 MMDIVQDATFYATLQTAHYHRDAGLPVLYEPEHHARGII-VKPRTDGADHDEMVFLLF 498  
 Db 402 LDMFSDVFFGIPAVLMSRLRDAFTYMYEYQYPSFVSVDORPQTVQGDHDEIFSVF 461  
 Qy 499 GGPFPATGLSMGKKEKALSQMKWYANFARTGNPDGNLPCWPRYNKDEKYLQDFTTRVG 558  
 Db 462 GTPFLKEGASBEEITNLSKWKWFWANFARNGNPNRGLPHWPQYDQKEEVLQIGATTQOA 521  
 Qy 559 MKLKEKMAFWMSLYQSORPEKQ 581  
 Db 522 QRLKAEVAFWTELLAKNPPQTE 544

RESULT 10  
 A31584  
 Carboxylesterase (EC 3.1.1.1) precursor - rat (fragment)  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 21-May-1990 #sequence\_revision 03-Aug-1992 #text\_change 18-Jun-1999  
 C:Accession: A31584  
 R: Long, R.M.; Satoh, H.; Martin, B.M.; Kimura, S.; Gonzalez, F.J.; Pohl, L.R.  
 Biochem. Biophys. Res. Commun. 156, 866-873, 1988  
 A:Title: Rat liver carboxylesterase: cDNA cloning, sequencing, and evidence for a multigene family  
 A:Reference number: A31584; MUID:89050119; PMID:2973315  
 A:Accession: A31584  
 A:Molecule type: mRNA  
 A:Residues: 1-540 (LON)  
 A:Cross-references: GB:M20629; GB:X13587; NID:G203279; PIDN:AAA40871.1; PID:G203280  
 C:Superfamily: cholinesterase; cholinesterase homology  
 C:Keywords: carboxylic ester hydrolase; glycoprotein  
 F:1-9/Domain: signal sequence #status predicted <SIG>  
 F:10-540/Product: carboxylesterase #status predicted <MAT>  
 F:41-529/Domain: cholinesterase homology <CHE>  
 F:70,265,266,293,366,467/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:212,444/Active site: Ser, His #status predicted

Query Match 35.9%; Score 1149; DB 2; Length 540;  
 Best Local Similarity 43.8%; Pred. No. 4e-85;  
 Matches 237; Conservative 96; Mismatches 188; Indels 20; Gaps 8;

Qy 46 HTKRPQVW-TKYGTLOGKQHV-GKT-PIQVFLGVPSRPPPLGILRFAPPEPPKIR 102  
 Db 10 HPSSPPVVDVTTKGVLGVLSLEGFTQPVAVFLGVPAKPPGLSLRFPAPPEPMSFVK 69  
 Qy 103 DATYFPCCLOES--WGQLASMYVSTRERYKWLRFSEDCLYNVYAPARAGDPQPLPVWV 161  
 Db 70 NTTYPPMCSQDGVVGGKLLDMLSTGKESIPLEFSEDCLYNIYSPADLTNKSRLPVMVW 129  
 Qy 162 PPGAFIVGAASSYEGSDLAAREKVVVFLQHRIGIFGFTDSDSHARGNWGLDQKVAL 221  
 Db 130 IHGGGLIIGGASPSYGLSALSAHENVVVTIYRLFGGGLFSTGDEHSRGNWGLDQKVAL 189  
 Qy 222 RWQENIAAFGDPGNVTLFGOSAGAMSISGLMSPLASGLFHRALISQSGTALFRLITS 281  
 Db 190 RWQDNIAFGDPGNVTFGESAGGFSVSLVLSPLAKNLFHRAISESGVLLTNDLKK 249  
 Qy 282 NPLKVAKVLAHAGNHNSTOILVNCRLALSGLTKMRVSNKMRFLQNFORDPEEIIWMS 341

Db 250 NTQAVAQMIATSGCNNTSSAAMVQCLRQ-----KTEAEELLETVKLDNT-----SM 296  
Qy 342 SPVVDGVVDDPLVLLTQGVSSVPYLLGVNLEFNWLLPYINKPLRQAMRKETIYK 401  
Db 297 STVIDGVLLPTEPEILITKSENFVPIVGFNKQEFGWIIPTWGNLLSSEGRNNEKVAS 356  
Qy 402 MLMSTRLLNITKEQVPLVVEEYLDNVEHDWMLNRMDIYQDATFVYATIQTAHYHR 461  
Db 357 FLKRFSPNLNISESVIPIAIEKYLGRGDDPAKK--KELLDDMFSDVFFGIPAVLMSLSJR 414  
Qy 462 DAGLPVLYIEFHHARGII-VKPRTDGADGDEMYFLFGGPPATGLSMGKEKALSQMMK 520  
Db 415 DAGAPTMYEFQVAPSPVSQRPQTQVGDHGEIFSVFGTFPLKEGASEEETNLSLVMK 474  
Qy 521 YWANFARTGNPDGMLPCWPRYNKDEKYLQDFTTRVGMKLKEKMAFWMSLYQSQRPEK 580  
Db 475 FWANFARNGPNNGEGLEPHWPKYDQEGYLQIGATTQQAQKLKGEVAFWTELLAKPPQT 534  
Qy 581 Q 581  
Db 535 E 535  
  
RESULT 11  
A39060  
carboxylesterase (EC 3.1.1.1) precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Mar-1992 #sequence\_revision 06-Mar-1992 #text\_change 18-Jun-1999  
C:Accession: A39060  
R:Ovnic, M.; Tepperman, K.; Medda, S.; Elliott, R.W.; Stephenson, D.A.; Grant, S.G.; Gar  
Genomics 9, 344-354, 1991  
A:Title: Characterization of a murine cDNA encoding a member of the carboxylesterase mul  
A:Reference number: A39060; MUID:91169540; PMID:1840565  
A:Accession: A39060  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-554 <OVN>  
A:Cross-references: GB:M57960; NID:g192853; PIDN:AAA63297.1; PID:g192854  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase  
F:50-540/Domain: cholinesterase homology <CHE>  
F:221,455/Active site: Ser, His #status predicted  
  
Query Match 36.7%; Score 1141.5; DB 2; Length 554;  
Best Local Similarity 41.5%; Pred. No. 1.7e-84;  
Matches 233; Conservative 113; Mismatches 190; Indels 25; Gaps 10;  
  
Qy 26 WI--LCW-SLTLCLMAQTAL-GALHTKRPQVVTYGTTLQGMHVGTPIQVFLGVPPS 80  
Db 2 WLHALVWASLAVCPILGHSLLPPVDTTQGVKLGKISLEGFEQ-----PVAVFLGVPPA 56  
  
Qy 81 RPLGLILRFAPPPPEPWKGIKIRATYTPPCLOES-WGQLASMYVSTRERYKWLRFSEDC 139  
Db 57 KPFLGSLRFAPQPAEFWSFKVNTATYPPNCSQDAGWAKILSDMFSTEKEILLPLKISEDC 116  
  
Qy 140 LYLVNYPAPARAPGDPOLPVNWFPGGAFIVGAASSYEGSDLAAREKVLVFLQRLGIFG 199  
Db 117 LYLVNISPDLTKSSQLPVNWNTHGGGLVIGRSPNGLSAHEVNVVTIYQRLGIGW 176  
  
Qy 200 FLSTDOSHARGNGLLDQMAALRWQENTAAFGDPPGNVTLPQSGAGAMSISGLMMSPLA 259  
Db 177 LFTSGDESHSPGNWAHLQDLAALRWQDNTANFGNPDSTVTFGESSGGISVSVLVLSPLG 236  
  
Qy 260 SGLFPHRAISOGTALFRLFTITSPLKAVKVAHLACGNHNSSTOILVNCRLALSIGTKWREV 319  
Db 237 KDLFPHRAISEGVVNTNVGKNQIQAVNEIIATLSQCNNTSSAAMVQCLRQKTESLELBI 296  
  
Qy 320 SNKMRFLQLNFORDPDEEIIWMSFPVVDGVVIPPDDPLVLLTQGVSSVPYLLGVNLEFNW 379  
Db 297 SGKLL--VQYNI-----SLSTMIDGVVLKPAPEEILAEKSFNTVPIVGFNKQEFCK 345  
  
Qy 380 LLPYINKPLNRQAMRKETITKMLMSTRLLNITKEQVPLVVEEYLDNVEHDWMLNR 439

Db 346 IIPMQLNLLPEGKNNEETASLLRRFHSNELNISSEMIPIAVIEQVLRGVDDPAKK--SEL 403  
Qy 440 MMDIVQDATFVYATIQTAHYHRDAGLPVLYIEFHHARGIIVK-PRTDGADGDEMYPLF 498  
Db 404 ILDMFGDIFFGIPAVLLSRSLRDAGVSTMYEFYRPSFVSQDKRPQTVEGDHGBIFPVF 463  
Qy 499 GQPPFATGLSMGKEKALSQMMKYNANPARTGNPDGMLPCWPRYNKDEKYLQDFTTRVG 558  
Db 464 GAPLLKEGASEEETNLSQMMKFWANFARNGPNNGEGLEPHWPEYDEQEGYLQIGATTQQA 523  
Qy 559 MKLKEKMAFWMSLYQSQRPE 579  
Db 524 QRLKAEVAFWTELLAKNPPE 544  
  
RESULT 12  
A29923  
carboxylesterase (EC 3.1.1.1), TCCD-induced 60K microsomal - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 08-Dec-1988 #sequence\_revision 08-Dec-1988 #text\_change 21-Aug-1998  
C:Accession: A29923; A29471  
R:Korza, G.; Ozols, J.  
J. Biol. Chem. 263, 3486-3495, 1988  
A:Title: Complete covalent structure of 60-kDa esterase isolated from 2,3,7,8-tetrachlo  
A:Reference number: A29923; MUID:88139431; PMID:3343253  
A:Accession: A29923  
A:Molecule type: protein  
A:Residues: 1-539 <KOR>  
R:Ozols, J.  
J. Biol. Chem. 262, 15316-15321, 1987  
A:Title: Isolation and characterization of a 60-kilodalton glycoprotein esterase from l  
A:Reference number: A29471; MUID:88033124; PMID:3667634  
A:Accession: A29471  
A:Molecule type: protein  
A:Residues: 1-71;193-208;436-446;532-539 <OZO>  
C:Superfamily: cholinesterase; cholinesterase homology  
C:Keywords: carboxylic ester hydrolase; endoplasmic reticulum; glycoprotein  
F:32-526/Domain: cholinesterase homology <CHE>  
F:61,363/Binding site: carbonyl group (Asn) (covalent) #status experimental  
F:195,441/Active site: Ser, His #status experimental  
  
Query Match 36.4%; Score 1133; DB 2; Length 539;  
Best Local Similarity 41.3%; Pred. No. 8e-84;  
Matches 227; Conservative 115; Mismatches 177; Indels 30; Gaps 10;  
  
Qy 46 HTRKPPQVVTYGTTLQGMHVGT-----TPIQVFLGVPPSPPLGILRFAPPEPPEP 97  
Db 1 HPSAPPVV---DTVKGKVL--GKTVSLGEGPACPVAVFLGVPPFAKPLGSLRFAPPPQPAES 55  
  
Qy 98 WKGIRDATTYPGCLQEB--SWGQLASMYVSTRERYKWLRFSEDCLYLVNYPAPARAPGDPQ 155  
Db 56 WSHVKNNTTSYPPMCCSSDAVSGHMLSELTNRKENIP-LKFSSEDCLYLVNYPADLTNRGR 114  
  
Qy 156 LPVNVWFPGGAFIVGAASSYEGSDLAAREKVLVFLQRLGIFGFLSTDSSHARGNWL 215  
Db 115 LPVNVWHGGGLVVGASTYDGLSAHEVNVVTIYQRLGIGGFENIDE-----L 166  
  
Qy 216 DQMAALRWQENTAAFGDPPGNVTLPQSGAGAMSISGLMMSPLASGLIFHRAISOGTALF 275  
Db 167 FLVAVNRWQDNTANFGDPPGVTIFGESAGQSVSILLISPLTKNLFHRAISESGVALL 226  
  
Qy 276 RLFTITSPLKAVKVAHLACGNHNSSTOILVNCRLALSIGTKWRYVSNKMRFLQLNFORDP 335  
Db 227 SSLFRKNTKSLAEKIALTEAGCKTTTSVAVHCLRQKTEELMEVTLKMKFNALDLVGDPK 286  
  
Qy 336 EIIWMSFPVVDGVVIPPDDPLVLLTQGVSSVPYLLGVNLEFNWLLP-YIMKFFPLNRQAM 394  
Db 287 ENTAFLLTVIDGVLLKPAPEIYEKKYNMLPYVMVGINQEQEFGWIIIPQMLGYPLSEGL 346  
  
Qy 395 RKEITKVLNSTRLLNITKEQVPLVVEEYLDNVEHDWMLNRMDIYQDATFVYATL 454  
Db 347 DQKATELLMKSYPVNVSKELTPVATEKYLGITGDDPVKK--KDLFLDMLADLLFGVPSV 404



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QY 455 QTAYHRDAGLPVLYEFEHH-ARGIIVKPRDGDHGDMDYFLFGGPFATGLSGKKEKA 513
Db 405 NVARHRDAGAPTYMEYRYRPSFSDMRPKTVIGDHGEIDFISVLGAPFLKEGATEEETK 464
QY 514 LSLQMKYANFARTGNPDGNLPCWPRYKDKYLQDFTTRVGNKLEKCKKQAFWMSLY 573
Db 465 LSKWKYANFARNPNNGEGLPQWPAYDKYGLQIGATTQAAQKLDKEVAFWTELM 524
QY 574 --OSQREK 580
Db 525 AKBAARPRE 533

RESULT 13
JC5408
carboxylesterase (EC 3.1.1.1) - human
C:Species: Homo sapiens (man)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JC5408
R:Schwer, H.; Langmann, T.; Daig, R.; Becker, A.; Aslanidis, C.; Schmitz, G.
Biochem. Biophys. Res. Commun. 233, 117-120, 1997
A:Title: Molecular cloning and characterization of a novel putative carboxylesterase, p
A:Reference number: JC5408; MUID:97289502; PMID:9144407
A:Accession: JC5408
A:Molecule type: mRNA
A:Residues: 1-559<SCH>
A:Cross-references: GB:Y09616; NID:G2058317; PIDN:CAA70831.1; PID:G2058318
A:Experimental source: intestine
C:Comment: This enzyme hydrolyzes many xenobiotics, such as carboxyl esters, thioesters
C:Genetics:
A:Gene: GDB:CEB2; iCB; CE2
A:Cross-references: GDB:9959011
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase; glycoprotein
F:58-544/Domain: cholinesterase homology <CHE>
F:13-95,123-280,291-428/Disulfide bonds: #status predicted
F:111,276/Binding site: carbohydtrate (Asn) (covalent) #status predicted
F:228,457/Active site: Ser, His #status predicted

Query Match 34.8%; Score 1083; DB 1; Length 559;
Best Local Similarity 40.8%; Pred. No. 9.6e-80;
Matches 232; Conservative 94; Mismatches 204; Indels 38; Gaps 10;

QY 27 ILCSLTLCLMAQTALGALHTKRPQVVKYGTGLQGMHV--GKTPIQVFLGVPPSRPL 84
Db 13 VACGLLLVRGQ---GDSASPIRTHTTQVGLSLVHVKGANAGVQTFLGIRFAKPL 68
QY 85 GILRFAPPEPEPWKGIKRDATTYPGCLQESWGQSLASMYVSTRERYKRLRFSEDCILYLV 144
Db 69 GILRFAPPEPEPWKGIKRDATTYPGCLQESWGQSLASMYVSTRERYKRLRFSEDCILYLV 128
QY 145 YAPARAPGDPQLPVMWFFPGCAFIVGAASVEGSDLAAREKVVFLQRLGIFGLSTD 204
Db 129 YTPAHSHEGSLNLPVMWVHGGALVFGMASLYDGSMLAALNVVWVVIQYRLGVLFSTG 188
QY 205 DSHARGNGLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMWPLASGLPH 264
Db 189 DKATGNWGLDQVAAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMWPLASGLPH 248
QY 265 RAISQSQTALFRFITSNPLKVAHVLAAGCNHNSTQILVNCRLSALSGTKVMYSNQR 324
Db 249 GAINESGVALLPGLIASSADVISTVWNTSACQVDSEALVGLCLRGKSEELINKPKF 308
QY 325 FLQNFORDPEEIIWMSPPVWVGWIPDDPLVLLTGQKVSVPYLLGVNLLPFI 384
Db 309 MI-----PGVVDGVFLPRHPQELLASADFPQVPSIVGVNNEFGWLIPIKY 353
QY 385 MKFPLNQARKKETITKMLNSTRTLLNITKEQVPLVVEEYL-DNVNEHDKMLRNRMMDI 443
Db 354 MRIYDTQKEMDREASQAALQKMLTLLMPTTFGLLREEYIGN---GDPQTLQAQFQM 410
QY 444 VQDATFYATLQTAHYHRDAGLPVLYEFEHHARGI-IVKPRDGDHGDMDYFL-----F 498

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Db 411 MADSMFVIPALOVAHF-QCSRAPVYFVFOHQPSWLKNIRPPHMKADHGDDELFFVRSFF 469
QY 499 GGPATGLSGKKEKALSLQMKYANFARTGNPDGNLPCWPRYKDKYLQDFTTRVG 558
Db 470 GGNVIKETE--EEQLSRKKMKYANFARNPNNGEGLPWPLFDOBEQYLLQNLQPAVG 527
QY 559 MKLKEKMAFW-----MSLYQSQRPEKQ 581
Db 528 RALKAHRLQFWKCALPKQIQELEPEER 555

RESULT 14
S47655
carboxylesterase (EC 3.1.1.1) precursor - golden hamster
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 26-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 20-Jun-2000
C:Accession: S47655
R:Stone, T.; Isobe, M.; Takabatake, E.; Wang, C.Y.
Biochim. Biophys. Acta 1207, 138-142, 1994
A:Title: Cloning and sequence analysis of a hamster liver cDNA encoding a novel putative
A:Reference number: S47655; MUID:94318665; PMID:8043605
A:Accession: S47655
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-561<SON>
A:Cross-references: EMBL:D28566; NID:G531238; PIDN:BAA05913.1; PID:G531239
C:Superfamily: cholinesterase; cholinesterase homology
C:Keywords: carboxylic ester hydrolase
F:58-546/Domain: cholinesterase homology <CHE>
F:227,459/Active site: Ser, His #status predicted

Query Match 34.1%; Score 1060; DB 2; Length 561;
Best Local Similarity 41.1%; Pred. No. 7.1e-78;
Matches 234; Conservative 97; Mismatches 191; Indels 48; Gaps 14;

QY 29 CWSLTLCLMAQTALGALH---TKRPQVVKYGTGLQGMHV--GKTPIQVFLGVPPSRPP 83
Db 8 CWRVAVACGLLLLVHVHGQDSVSPINHTTQVGRKLVVYKGVGVVAFIPIPAKPP 67
QY 84 LGILRFAPPEPEPWKGIKRDATTYPGCLQESW--GOLASMYVSTRER---YKWLRFSD 138
Db 68 VGLRFAPPEPEPWKGIKRDATTYPGCLQESW--GOLASMYVSTRER---YKWLRFSD 121
QY 139 CLYLVNYPARAPGDPQLPVMWFFPGCAFIVGAASVEGSDLAAREKVVFLQRLGIF 198
Db 122 CLYLVNYPARAPGDPQLPVMWFFPGCAFIVGAASVEGSDLAAREKVVFLQRLGIF 181
QY 199 GFLSTDSDSHARGNGLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMWSP 258
Db 182 GFLSTDSDSHARGNGLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMSISGLMWSP 241
QY 259 ASGLFHRARISQSGTALFRFITSNPLKV-AKKVAHLACGNHNSTQILVNCRLSALSGTKVM 317
Db 242 SKGLFHGAIMQSGVALLPDLISDTPEAVYTFVWVANOQSGCEAKDSEALVHCLREKTBAIL 301
QY 318 RVSNKMRFLQNFORDPEEIIWMSPPVWVGWIPDDPLVLLTGQKVSVPYLLGVNLE 376
Db 302 AINQ-----VFINTPGVVDGIFLPRHPQELLASVDHPVPSIIGVDSDE 345
QY 377 FNWLLPYMKFPLNQARKKETITKMLNSTRTLLNITKEQVPLVVEEYLDNVNEHDKML 436
Db 346 CGWGVPLFMGLDHIKNTITRETLPAFLKRAEHNMLPPECSDLLMQEYMGDV--EDPQTL 403
QY 437 RNRWMDIVQDATFYATLQTAHYHRDAGLPVLYEFEHHARGI---IVKPRDGDHGD 493
Db 404 QAQFRELKMDPMFVLPALKVAYFOR-SHAPVYFVFOHQSFINKDKDARSHVRADHGDH 462
QY 494 MYFLFGGPFATGLSMG---KEKALSQMKYANFARTGNPDGNLPCWPRYKDKYLQ 550
Db 463 VAFVFGSDF-WGLKIDLITEEKLKRMKMYANFARNPNNGEGLPWPLVHDDQYLK 521
QY 551 LDFTRVGMKLEKMAFWMSLYQSQRPEK 580

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Search completed: August 3, 2004, 22:28:52  
Job time : 23 secs



Result No.	Query	Score	Match	Length	DB	ID	Description
1	1290.5	41.5	557	1	SASB	ANAPL	Q04791 anas platyr
2	1259	40.5	565	1	ES10	RAT	P16303 rattus norv
3	1251	40.2	567	1	EST1	HUMAN	P23141 homo sapien
4	1239.5	39.8	566	1	EST1	P1G	Q29550 sus scrofa
5	1205.5	38.7	561	1	EST3	RAT	Q63108 rattus norv
6	1205.5	38.7	562	1	ES22	MOUSE	Q64176 mus musculus
7	1187.5	38.2	561	1	EST5	RAT	Q63010 rattus norv
8	1184.5	38.1	561	1	EST4	RAT	P16303 rattus norv
9	1161.5	37.3	549	1	EST1	RAT	P10959 rattus norv
10	1141.5	36.7	554	1	ESTN	MOUSE	P23953 mus musculus
11	1133	36.4	539	1	EST1	RABIT	P12337 oryctolagus
12	1060	34.1	561	1	EST1	MESAU	Q64419 mesocricetu
13	1034	33.2	554	1	ESTN	MOUSE	P36880 mus musculus
14	993	31.9	532	1	EST2	RABIT	P14943 oryctolagus
15	849	27.3	836	1	NLG2	RAT	Q62888 rattus norv
16	847	27.2	835	1	NLG2	HUMAN	Q8nf24 homo sapien
17	831	26.7	848	1	NLG3	RAT	Q62889 rattus norv
18	820.5	26.4	848	1	NLG3	HUMAN	Q9nz94 homo sapien
19	819.5	26.3	825	1	NLG3	MOUSE	Q8dym5 mus musculus
20	800	25.7	816	1	NLG4	HUMAN	Q8nf04 homo sapien
21	797	25.6	816	1	NLG4	HUMAN	Q8nf23 homo sapien
22	788	25.3	843	1	NLG1	RAT	Q62765 rattus norv
23	787.5	25.3	840	1	NLG1	HUMAN	Q8nf27 homo sapien
24	787	25.3	814	1	ACES	HUMAN	P22303 homo sapien
25	785	25.2	843	1	NLG1	MOUSE	Q99x10 mus musculus
26	776.5	25.0	611	1	ACES	FELCA	Q62763 felis silve
27	770	24.7	613	1	ACES	BOVIN	P23795 bos taurus
28	761.5	24.5	614	1	ACES	MOUSE	P21836 mus musculus
29	757	24.3	606	1	ACES	BUNFA	Q92035 bungarus fa
30	757	24.3	633	1	ACES	ELEBEL	Q43275 electrophor
31	751.5	24.1	584	1	ACES	RABIT	Q29499 oryctolagus
32	751.5	24.1	614	1	ACES	RAT	P37136 rattus norv
33	728	23.4	612	1	CEL	RAT	P07882 rattus norv

CC	EMBL; L05493; AAA49223.1; -.	
DR	PIR; A47162; A47162.	
DR	HSP; P37967; 1OE3.	
DR	InterPro; IPR002018; CarbesteraseB.	
DR	InterPro; IPR000379; Ser esters.	
DR	Fam; PF00135; Coesterase; 1	
DR	PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.	
DR	PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.	
KW	Fatty acid biosynthesis; Hydrolase; Signal.	
FT	SIGNAL	1 25
FT	CHAIN	26 557
FT	DISULFID	93 122
FT	ACT SITE	227 227
FT	ACT SITE	345 345
FT	ACT SITE	460 460
FT	FATTY ACYL-COA HYDROLASE.	
FT	BY SIMILARITY.	
FT	BY SIMILARITY.	
FT	BY SIMILARITY.	
FT	BY SIMILARITY.	

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FT CARBOHYD 476 476 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 557 AA; 61637 MW; 03E3D90A037F6B0 CRC64;

Query Match 41.5%; Score 1290.5; DB 1; Length 557;
Best Local Similarity 46.0%; Pred. No. 4.8e-95;
Matches 260; Conservative 106; Mismatches 172; Indels 27; Gaps 11;

QY 27 ILWSLTILCLMAQTALGHTKRPQVTKYCTLOGKQHV--GKTPQVGLGVPRRPPL 84
D 8 LLSLITAGTALVATQ--RAEQEVVNTGSGVGYQVKNAAERSVNVFLGPFAPKPV 66
QY 85 GILFAPPEPPEPWKGIARDATTPPGCLOES--WGOLASMYVSTRERYKMLRFSEDCLYLN 143
D 67 GPLRFSPPQPEPWKGVDRDAASYPMLCQKVLQGYLSDAITNRKEKVRQLQISEDCLYLN 126
QY 144 VYAPARAPGDPQPLPVMVTFPGGAFIVCAASYSYSGSDLAAREKVLVFLQHRIGIFGLST 203
D 127 VYTPVSTEEQELPVPVFIHGGGLVSGAASSYDGSALAFDNVVVVIQYRLGIAGYFT 186
QY 204 DSHARGNGLLDQMAALRWQENIAAFGDPGNVTILFGQAGAMSGISGLMSPLASGLF 263
D 187 GDXHARGNGLVDQVAALQWQENIHFRCDPGVTIFGESAGSVSALVLSPLAKGLF 246
QY 264 HRAISQSTALFRLFTSNPLKVAKVHLAGNHSTQILLNCLRALSGTKVMRVSNRM 323
D 247 HKAISEGTAV--RLFTPEQPEBQARIAAAGCEKSSAALVECLREKTEAEMEQTILRM 305
QY 324 RFLQNFQRPDEETIIMSPPVQGVVDPDPLVLTGKVSVPYLLGVNNLEFNWLLPY 383
D 306 -----PPWFI-----SASLDGVFPKPSPROLLSEKVINAVPYIIGVNNCEFGHILPR 352
QY 384 IMKPLNRQARVETITKMLWSTRL--LNIITKEQVPLVVEEYLDNVNHDWMLNRNM 441
D 353 MKRFPPETEGLEKDVARQLQSTLALSFKGAPSDIVDLVVEYI--GVAENR--AQVRDGLL 410
QY 442 DIVQDAPVATQTAHYHREDAGLPVLYEFEEH--ARGIIVKPRTDGADGDEMFLF 498
D 411 DSTADPLFVSVEVAVRHHDAGNPVYFQHRPSSAGV--PFFVADHADAETAFV 468
QY 499 GGPATGLSKGKALKSLQMKYKWMANFARTGNPDGNLPCWPRYNKDEKYLQIDETTRVG 558
D 469 GKPFPLAGNATEEBEAKLSRTVMKWTNFAANGNPNGBGLVHPQYDMDERYLIDLTQRA 528
QY 559 MKLKEKQWAFMSLYQSQRPEKQ 583
D 529 KKLKERKQWFMQLTSQIMSDRRK 553

RESULT 2
ES10 RAT
ID ES10 RAT STANDARD; PRT; 565 AA.
AC P16303; Q64574;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Liver carboxylesterase 10 precursor (EC 3.1.1.1) (Carboxylesterase ES-10) (PI 6.1 esterase) (ES-HVEL).
OS Rattus norvegicus (Rat)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley, and Wistar; TISSUE=Liver;
RX MEDLINE=90351366; PubMed=2386485;
RA Robbi M., Beaufay H., Octave J.-N.;
RT "Nucleotide sequence of cDNA coding for rat liver pi 6.1 esterase (ES-10), a carboxylesterase located in the lumen of the endoplasmic reticulum.";
RL Biochem. J. 269:451-458(1990).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;

```

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RX MEDLINE=92299008; PubMed=1606962;
RA Medda S., Proia R.L.;
RT "The carboxylesterase family exhibits C-terminal sequence diversity reflecting the presence or absence of endoplasmic-reticulum-retention sequences.";
RL Eur. J. Biochem. 206:801-806(1992).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=96130267; PubMed=8541339;
RA Ghosh S., Mallonee D.H., Hylemon P.B., Grogan W.M.;
RT "Molecular cloning and expression of rat hepatic neutral cholesteryl ester hydrolase.";
RL Biochim. Biophys. Acta 1259:305-312(1995).
CC -!- FUNCTION: PROBABLY INVOLVED IN THE METABOLISM OF XENOBIOTICS AND OF NATURAL SUBSTRATES.
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a carboxylic anion.
CC -!- SUBUNIT: Homotrimer.
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC -----
DR EMBL; X51974; CAA3236.1; -
DR EMBL; X65296; CAA46391.1; -
DR EMBL; L46791; AAA88507.1; -
DR HSP; P21836; 1VAA.
DR InterPro; IP002018; CarbesteraseB.
DR InterPro; IP000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Serine esterase; Glycoprotein; Endoplasmic reticulum;
KW Signal; Multigene family.
FT SIGNAL 1 18
FT CHAIN 19 565 LIVER CARBOXYLESTERASE 10.
FT ACT_SITE 221 221 BY SIMILARITY.
FT ACT_SITE 353 353 BY SIMILARITY.
FT ACT_SITE 466 466 BY SIMILARITY.
FT DISULFID 87 116 BY SIMILARITY.
FT DISULFID 273 284 BY SIMILARITY.
FT SITE 562 565 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 79 79 N-LINKED (GLCNAC... ) (POTENTIAL).
FT CARBOHYD 489 489 N-LINKED (GLCNAC... ) (POTENTIAL).
FT VARIANT 186 186 R -> Q (IN SPRAGUE-DAWLEY).
FT VARIANT 265 265 K -> N (IN SPRAGUE-DAWLEY).
FT VARIANT 423 423 I -> M (IN SPRAGUE-DAWLEY).
FT VARIANT 506 506 S -> N (IN SPRAGUE-DAWLEY).
FT CONFLICT 420 420 A -> E (IN REF. 3).
FT CONFLICT 491 492 SK -> TQ (IN REF. 3).
SQ SEQUENCE 565 AA; 62144 MW; F973AF2A71CC1F84 CRC64;

Query Match 40.5%; Score 1259; DB 1; Length 565;
Best Local Similarity 43.0%; Pred. No. 1.6e-92;
Matches 241; Conservative 120; Mismatches 182; Indels 18; Gaps 6;

QY 28 LCHSLTILCLMAQTALG-----ALHKRPQVTKYCTLOGKQHVCKTPIQVFLGVPR 81
D 6 LVW---LFLAACTAWGYPSPVNTVTKGKGVNLEGFAQ-----EVAFLGIPFAK 57
QY 82 PPLGILRFAPPEPPEPWKGIARDATTPPGCLOES--WGOLASMYVSTRERYKMLRFSEDC 140
D 58 PPLGSLRFRAPPQPAEPWNVFQNTTSYPPMCSQDVGQVLSLFTNRKNIFLQFSEDC 117
QY 141 YLNYAPARAPGDPQPLPVMVTFPGGAFIVCAASYSYSGSDLAAREKVLVFLQHRIGIF 200

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Db 118 YLNVYTPADLTNKSRLPVMWVHGGGLVVGASTYDGOVLSAHENVVVVTTQYRLGNGP 177  
QY 201 LSTDSDSHARGNGLLDQMAALRWQENIAAFGGDPGNVTLFQSGAGAMSISGLMMSPLAS 260  
Db 178 FTGDESHSGNWHLDQVAALHWQDNIANFGNPGSVTFIFESAGGSVSALVLSPLAK 237  
QY 261 GLPHRAISOGTALPFLFTSNTPLKVAKKVAHLACGNHNSTOILVNCRLRALSGTKMVRVS 320  
Db 238 NLFHRAISESGVVLTSALITDSKPIAKLIATLSGCKTTTSAMVHCLRQKTEDELLETS 297  
QY 321 NKGRFLQALQFQDPPEIINWSMSPVVDGVIIPDPLVLLTQGVSSVPYLLGVNNLEENWL 380  
Db 298 LKLNLFKLLGNPKESYFPLFTVIDGVLPKTPPEILAEKSNFVPIVINGINKBFGWI 357  
QY 381 LPYIMKPPNLRQAMKXETITKMLWSTRLTNITKQVPLVBEYLDNVDNHEHDKMLNRNM 440  
Db 358 IPTLMGYPLSEGKLDQKAKSLKWSYPTLKISEKMPVVAEKYFGGTD--DPAKRKDLF 415  
QY 441 MIVQDQATFYATLOTAYHRDAGLPVLYEYEHARGI-IVKPRDGDADHDENVYFLFG 499  
Db 416 QDLVADVIFGVSPVWSRHRDAGAPTFWYEYFPRFSVSAWRPKTVIGDHGDELFSVFG 475  
QY 500 GPFATGLSGKKEKALSLQWVKYWANFARTGNPDGNLPCWPRYNKDEKYLQDLFTTRYGM 559  
Db 476 SPLKDGASEEETNLKWKYKWFANFARNGSPNGGGLPHWPEYDQKEGYLKIGASTQAAQ 535  
QY 560 KLKEKQVAFWMSLYQSRPEK 580  
Db 536 RLKDKVAFWSELRAKEAAEE 556  
RESULT 3  
ESTL\_HUMAN STANDARD; PRT; 567 AA.  
AC P23141; Q00015; Q13657; Q14062; Q16737; Q16788; Q9JULY2;  
DT 01-NOV-1991 (Rel. 20, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DE 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Liver carboxylesterase precursor (PC 3.1.1.1) (Acyl coenzyme  
esterase) (HWE) (Serine esterase) (ACAT) (Monocyte/macrophage serine  
CES1 OR CES2 OR SES1)  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
SEQUENCE FROM N.A.  
RX MEDLINE=92011649; PubMed=1918003;  
RA Munger J.S., Shi G.P., Mark E.A., Chin D.T., Gerard C.,  
Chapman H.A.;  
RT "A serine esterase released by human alveolar macrophages is closely  
related to liver microsomal carboxylesterases.";  
RL J. Biol. Chem. 266:11832-11838(1991).  
RN [2]  
SEQUENCE FROM N.A.  
RX MEDLINE=94032283; PubMed=8218228;  
RA Kroetz D.L., McBride O.W., Gonzalez F.J.;  
RT "Glycosylation-dependent activity of baculovirus-expressed human  
liver carboxylesterases: cDNA cloning and characterization of two  
highly similar enzyme forms.";  
RL Biochemistry 32:11606-11617(1993).  
RN [3]  
SEQUENCE FROM N.A.  
RC TISSUE=Peripheral blood, and Placenta;  
TX MEDLINE=94010913; PubMed=8406473;  
RX Shibata F., Takagi Y., Kitajima M., Kuroda T., Omura T.;  
RT "Molecular cloning and characterization of a human carboxylesterase  
gene.";  
RL Genomics 17:76-82(1993).  
RN [4]  
SEQUENCE FROM N.A.  
RP

RC TISSUE=Liver;  
RX MEDLINE=94325258; PubMed=8049197;  
RA Becker A., Bottcher A., Lackner K.J., Fehringer P., Norka F.,  
Aslanidis C., Schmitt G.;  
RT "Purification, cloning, and expression of a human enzyme with acyl  
coenzyme A: cholesterol acyltransferase activity, which is identical  
to liver carboxylesterase.";  
RL Arterioscler. Thromb. 14:1346-1355(1994).  
RN [5]  
SEQUENCE OF 1-429 FROM N.A.  
RP TISSUE=Brain;  
RX MEDLINE=99448370; PubMed=10518925;  
RA Mori M., Hosokawa M., Ogasawara Y., Tsukada E., Chiba K.;  
RT "cDNA cloning, characterization and stable expression of novel human  
brain carboxylesterase.";  
RL FEBS Lett. 458:17-22(1999).  
RN [6]  
SEQUENCE OF 61-567 FROM N.A.  
RP TISSUE=Liver;  
RX MEDLINE=91148424; PubMed=1997784;  
RA Long R.M., Calabrese M.R., Martin B.M., Pohl L.R.;  
RT "Cloning and sequencing of a human liver carboxylesterase isoenzyme.";  
RL Life Sci. 48:PL43-PL49(1991).  
RN [7]  
SEQUENCE OF 64-567 FROM N.A., AND PARTIAL SEQUENCE.  
RX MEDLINE=91300111; PubMed=2070086;  
RA Zschunke F., Salmassi A., Kreipe H., Buck F., Parwaresch M.R.,  
Radzun H.J.;  
RT "cDNA cloning and characterization of human monocyte/macrophage  
serine esterase-1.";  
RL Blood 78:506-512(1991).  
RN [8]  
SEQUENCE OF 114-567 FROM N.A.  
RP TISSUE=Liver;  
RX MEDLINE=92084150; PubMed=1749313;  
RA Riddles P.W., Richards L.J., Bowles M.R., Pond S.M.;  
RT "Cloning and analysis of a cDNA encoding a human liver  
carboxylesterase.";  
RL Gene 108:289-292(1991).  
CC -!- FUNCTION: Involved in the detoxification of xenobiotics and in the  
activation of ester and amide prodrugs. Hydrolyzes aromatic and  
aliphatic esters, but has no catalytic activity toward amides or a  
fatty acyl CoA ester.  
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a  
carboxylic anion.  
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.  
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
CC  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M73499; AAA35649.1; -  
DR EMBL; L07764; AAA16036.1; -  
DR EMBL; L07765; AAA35711.1; -  
DR EMBL; D21088; BAA04650.1; -  
DR EMBL; D21075; BAA04650.1; JOINED.  
DR EMBL; D21076; BAA04650.1; JOINED.  
DR EMBL; D21077; BAA04650.1; JOINED.  
DR EMBL; D21079; BAA04650.1; JOINED.  
DR EMBL; D21080; BAA04650.1; JOINED.  
DR EMBL; D21081; BAA04650.1; JOINED.  
DR EMBL; D21082; BAA04650.1; JOINED.  
DR EMBL; D21083; BAA04650.1; JOINED.  
DR EMBL; D21084; BAA04650.1; JOINED.  
DR EMBL; D21085; BAA04650.1; JOINED.  
DR EMBL; D21086; BAA04650.1; JOINED.  
DR EMBL; D21087; BAA04650.1; JOINED.  
DR EMBL; AB025025; BAA84995.1; -



KW Signal; Multigene family.  
 FT SIGNAL 1 18 BY SIMILARITY.  
 FT CHAIN 19 566 LIVER CARBOXYLESTERASE.  
 FT ACT\_SITE 222 222 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 467 467 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT DISULFID 88 117 BY SIMILARITY.  
 FT DISULFID 274 285 BY SIMILARITY.  
 FT SITE 563 566 PREVENT SECRETION FROM ER (POTENTIAL).  
 FT CARBOHYD 80 80 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 566 AA; BE046545307DEDE5 CRC64;  
 Query Match 39.8%; Score 1239.5; DB 1; Length 566;  
 Best Local Similarity 44.4%; Pred. No. 5.6e-91;  
 Matches 248; Conservative 110; Mismatches 192; Indels 11; Gaps 7;  
 QY 26 WILCWSLTLCLMAQTALGALHTKRPQVW-TKYGTLOGKQWVG--KTIQVFLGVFPFSP 82  
 DB 2 WLL--PLVLTSLASSATWAGQAPSPVDTAQRVLGVKYSLEGLAQPVAVFLGVFPFAP 59  
 QY 83 PLGILRAPPEPPKGIKRDATYPPGCIQESWGO--LASMYVSTRERYKMLRSEDCL 140  
 DB 60 PLGLSLAFAPQAPAPSPFVNTTSYPPMCCQDPVVEQMTSDLTNGKRLT-LFESDCL 118  
 QY 141 YLNVYAPAPGDPQLPVMVWPGGAFIVGAASSYEGSDLAAREKVVLFLOHRLGIFG 200  
 DB 119 YLNIYPADITKGRPLVMVWIHGGGLVLCGAPYDGVLAHENVVVAIQVRLGIFG 178  
 QY 201 LSTDDSHARGNGLLDQMAALRVQENIAAFGDPGNVTLFGOSAGAMSISGLMMSPLAS 260  
 DB 179 FSTGDEHSRGNWGLDQVAALHWQENIANFNGDPSGVTIFGESAGGESVSVLVLSPLAK 238  
 QY 261 GLFHRAISQSGTALFRITSNPLKVAKVHLAGCNHNSQLVNCRLASLSTKVMRVS 320  
 DB 239 NLFHRAISEGVALTVALKVKKWAAKQJAVLAGCKTTTSAVFVHCLQKSEDELDLT 298  
 QY 321 NKRFQLNQRDPEETIWSMSPVVDGVTIPDPLVLLTQGVSSVPYLLGVNNEFFNL 380  
 DB 299 LKMKELTLDPHGDORESHPLPTVVDGVLKPKMPEILAEKIDNTVPIVINGKQEFGL 358  
 QY 381 LPVIMKPLNQAMRKETITKMWSTRTLLNITKEQVPLVVEYLDNVNHEHDKMLNRM 440  
 DB 359 LPTMGFPFLEGGDKDOKTATSLWKSYPYIANIPEELTPVATDKYLGTDTPVKK--KDLF 416  
 QY 441 MDVQVQATFYVATLQAHYHRDAGLPVLYLVEFHH--ARGIIVKPRTDGADHGDVFLFG 499  
 DB 417 LDLMGVVFGVSVTVARQHRDAGATYMYEFOYRPSFSDKPKYVIGDHGDEIFSVFG 476  
 QY 500 GPATGLSMGKELSKALSMYKWFANFARTGNPDGNLPCWPRYNKDEKYLQDLDTTRVGM 559  
 DB 477 FPLLKGDAPPEEVSLSKTVMKFWANFARSNGPNEGGLPHWPMYDQEGVLIQVNTQAAK 536  
 QY 560 KLKEKKWAFWMSLYQSORPEK 580  
 DB 537 RLKGEVAFVNDLLSKEAAKK 557  
 RESULT 5  
 EST3 RAT ID\_EST3 RAT STANDARD; PRT; 561 AA.  
 AC Q63106;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Liver carboxylesterase 3 precursor (EC 3.1.1.1) (Carboxylesterase ES-3)  
 DE (pI 5.5 esterase) (ES-HTEL).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RX MEDLINE=95032008; PubMed=7945287;

RA Robbi M., Beaufay H.;  
 RT "Cloning and sequencing of rat liver carboxylesterase ES-3 (egasyn).";  
 RL Biochem. Biophys. Res. Commun. 203:1404-1411 (1994).  
 CC -!- FUNCTION: Involved in the detoxification of xenobiotics and in the  
 CC activation of ester and amide prodrugs.  
 CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a  
 CC carboxylic anion.  
 CC -!- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic  
 CC reticulum.  
 CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 CC  
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 CC  
 EMBL; X81395; CAA57158.1; -;  
 PIR; JC2447; JC2447.  
 HSSP; P21836; IMAA.  
 InterPro; IPR002018; Carbesterase8.  
 InterPro; IPR003379; Ser esters.  
 Pfam; PF00135; Coesterase\_1.  
 PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;  
 KW Signal; Multigene family.  
 FT SIGNAL 1 18 BY SIMILARITY.  
 FT CHAIN 19 561 LIVER CARBOXYLESTERASE 3.  
 FT ACT\_SITE 221 221 BY SIMILARITY.  
 FT ACT\_SITE 466 466 BY SIMILARITY.  
 FT DISULFID 87 116 BY SIMILARITY.  
 FT DISULFID 273 284 BY SIMILARITY.  
 FT SITE 558 561 PREVENT SECRETION FROM ER (POTENTIAL).  
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 107 107 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 489 489 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 561 AA; 61714 MW; 1E14D66DF098986F CRC64;  
 Query Match 38.7%; Score 1205.5; DB 1; Length 561;  
 Best Local Similarity 43.3%; Pred. No. 2.9e-88;  
 Matches 238; Conservative 114; Mismatches 191; Indels 7; Gaps 6;  
 QY 28 LC-WSLTLCLMAQTALGALHTKRPQVVTKYGTLOGKQWVG-KGT-PQVFLGVFPFSP 84  
 DB 1 MCLRALILVFLAAATAGGHPSSLPVDTLQGVKLVGSLEGTQPVAVFLGVFPFAP 60  
 QY 85 GILFAPFAPPEPPKGIKRDATYPPGCIQES-WGOLASMYVSTRERYKMLRSEDCLYN 143  
 DB 61 GSLFAPFAPQAPAPSPFVNTTSYPPMCCQDPVAGQIVNDLLTNWEENISLQFSEDCLYN 120  
 QY 144 VYAPAPGDPQLPVMVWPGGAFIVGAASSYEGSDLAAREKVVLFLOHRLGIFGFLST 203  
 DB 121 IYTPADLTKRDLPLVMVWIHGGGLVLCGASTYDGLALSTHENVVVVIQYRLGFWGFST 180  
 QY 204 DSHARGNGLLDQMAALRVQENIAAFGDPGNVTLFGOSAGAMSISGLMMSPLASGLF 263  
 DB 181 GDEHSRGNWGLDQVAALHWQENIDNFGDPSGVTIFGESAGGESVSVLVLSPLAKNLF 240  
 QY 264 HRAISQSGTALFRITSNPLKVAKVHLAGCNHNSQLVNCRLASLSTKVMRVSNM 323  
 DB 241 HKAISESGVALTAGLVKKNTRPLAEKIAVWSGCKSTTSASMVHCLQKTEBELLETLKL 300  
 QY 324 RFLQNFQDPEETIWSMSPVVDGVTIPDPLVLLTQGVSSVPYLLGVNNEFFNL 383  
 DB 301 NLFSLDLHGDGRQSPFPVPTVLDGVLVLPKMPPEILAEKIDNTVPIVINGKQEFGLPT 360  
 QY 384 IMKFLANRQAMRKETITKMWSTRTLLNITKEQVPLVVEYLDNVNHEHDKMLNRMDI 443  
 DB 361 MNVPPSPDKLDPMTATSLKSSFLNLPPEAIPVAEIKYLRHTDDPRN--KDQLLEL 418



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QY 444 VQATFVATLQTAHVHRDAGLPVLYVEFEHH-ARGIIIVKPRTDGADHGDGEMVFLFGPPF 502
Db 419 IGVIFGVPSVIVSRGHRDAGARTMYEQYRPSFSKMKPSTVVDGHDGEIYSVFGAPI 478
QY 503 ATGLSMGKELALQMKYKWFANFARTGNPDGNLPCWPRYNKDEKYLQDFTTRVGMK 562
Db 479 LRGTGSKKEEINLSKMMKFWANFARNPNQGLPHWPEYDQKEGYLQIGATTQQAQKLK 538
QY 563 EKKNAFMMSL 572
Db 539 EKEVAFWSEL 548

RESULT 6
ID ES22_MOUSE STANDARD; PRT; 562 AA.
AC Q64176;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase 22 precursor (EC 3.1.1.1) (Egagyn) (Esterase-22) (fs-22).
DE GN ES22.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=92147141; PubMed=1783403;
RA Oeintz N., Swank R.T., Fletcher C., Zhen L., Novak E.K., Baumann H.,
RA Heintz N., Ganschow R.E.;
RT "Characterization and functional expression of a cDNA encoding egagyn
RT (esterase-22): the endoplasmic reticulum-targeting protein of beta-
RT glucuronidase."
RL Genomics 11:956-967(1991).
CC -!- FUNCTION: Involved in the detoxification of xenobiotics and in the
CC activation of ester and amide prodrugs.
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -!- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
CC reticulum.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC
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CC
CC ENBL; S80191; AAB21335.1; -.
DR PIR: A55281; A55281.
DR HSP: P21836; 1MAH.
DR MGD; MGI:95432; ES22.
DR InterPro; IPR002018; CarboxylesteraseB.
DR InterPro; IPR000379; Ser_estr.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW Signal; Multigene family.
FT SIGNAL 19 BY SIMILARITY.
FT CHAIN 20 562 LIVER CARBOXYLESTERASE 22.
FT ACT SITE 222 222 BY SIMILARITY.
FT ACT SITE 467 467 BY SIMILARITY.
FT DISULFID 88 117 BY SIMILARITY.
FT DISULFID 274 285 BY SIMILARITY.
FT SITE 559 562 PREVENT SECRETION FROM ER (POTENTIAL).
FT CARBOHYD 80 80 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 276 276 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 490 490 N-LINKED (GLCNAC. .) (POTENTIAL).

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SQ SEQUENCE 562 AA; 61581 MW; F81A4367A0CCB2E3 CRC64;
Query Match 38.7%; Score 1205.5; DB 1; Length 562;
Best Local Similarity 42.4%; Pred. No. 2.9e-88;
Matches 241; Conservative 119; Mismatches 188; Indels 21; Gaps 9;
QY 28 LCWS-LTLCLMAQTALGALHTKEPQVVTYKGTILQGMHVGK-----TPIQVFLGVP 78
Db 1 MCLSALILVSLAFTAGAGHPSPPPV---DTVCGKVL--GKYISLEGFTQPVAVFLGVP 55
QY 79 FSRPFLGILRFAPPEPEPPKIGIRDATTYPPGCLQES-WQQLASMYVSTRERYKMLRFSE 137
Db 56 FAKPPLGLSLRFAPPEPAEPWSSVKNATSYPPMCFQDPVTGQIVNDLLTNKRKIPLOFSE 115
QY 138 DCLYLVNYAPARAPDPQLPVMWVFGGAFIVGAASSYEGSDLAAREKVLVFLQRLGI 197
Db 116 DCLYLVNIYTPADLTSTKSRLEPVMVWVHGGGLVLGASTYDGLVLTSTHENVVVVVIQRLGI 175
QY 198 FGFLSTDDSHARGNWGLLDQMAALRWQENIAAFGGDPGNVTLFGQSAGAMVSLGLMSP 257
Db 176 WGFSTGDEHSRGNWGHLDQVAALHWQDNIAKFGGDPGSGVTIFGESAGGESVSLVLS 235
QY 258 LASGLFHRAISQSGTALFRUITSNPLKVAKVLAHLAGCHNHNSTOILVNCRLALSTKVM 317
Db 236 LAKNLFQRAISEGVALTAGLVKNTPLAEKIAVISGCKNTTSAAMVHCLROKTEBELL 295
QY 318 RVSNKMFLOLNFORDPEEIIWSMSPVWDGWIWPDPLVLLTQCKVSSVPYLLGVNLEF 377
Db 296 GTTLKLNLFKLDLHGDSRQSHPFVPTVLDGLVLPKMPPEELAEKNFTVPIYVIGINKQEF 355
QY 378 NWLLPYINKPLNRQAMKRTITKMLSTETLITKEQVPLVVEYVLYDNVNEHDK-ML 436
Db 356 GWILPTWNTYPPSDVKLDQMTAMSLKSSFLNLPEDALIAVAIEKYL---RDKYTGREN 412
QY 437 RNRWMDIVQDATFYATVLTQTAHVHRDAGLPVLYVEFEHH-ARGIIIVKPRTDGADHGD 495
Db 413 KDQLELIGDGVVGVPSVIVSRGHRDAGARTMYEQYSPFSSEMKPDTVVDGHDGEIY 472
QY 496 FLFGGPPATGLSMGKELALQMKYKWFANFARTGNPDGNLPCWPRYNKDEKYLQDFTT 555
Db 473 SVFGAPILRGTSBEEINLSKMMKFWANFARNPNQGLPHWPEYDQKEGYLQIGATT 532
QY 556 RVGKLEKEMAFWMSLY-QSORPEKORQ 583
Db 533 QQAQKLEKEVAFWTELLAKKQLPTEHTE 561

RESULT 7
EST5_RAT
ID EST5_RAT STANDARD; PRT; 561 AA.
AC Q63010;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase B-1 precursor (EC 3.1.1.1) (Liver microsomal
DE carboxylesterase). (Rat).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=95050819; PubMed=7961958;
RA Yan B., Yang D., Brady M., Parkinson A.;
RT "Rat kidney carboxylesterase. Cloning, sequencing, cellular
RT localization, and relationship to rat liver hydrolase."
RL J. Biol. Chem. 269:29688-29696(1994).
CC -!- FUNCTION: Involved in the detoxification of xenobiotics and in the
CC activation of ester and amide prodrugs.
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -!- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic

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CC CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR DRL: U10698; AAA64639.1; -.
DR HSP; P21836; IMAA.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000886; ER_target_5.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW Signal; Multigene family.
FT SIGNAL 1 18
FT CHAIN 19 561
FT ACT_SITE 221 221
FT ACT_SITE 466 466
FT DISULFID 87 116
FT DISULFID 273 284
FT SITE 558 561
FT CARBOHYD 79 79
SQ SEQUENCE 561 AA; 62494 MW; 013C1C3ACEBCEC9 CRC64;
Query Match 38.2%; Score 1187.5; DB 1; Length 561;
Best Local Similarity 41.1%; Pred. No. 7.8e-87;
Matches 230; Conservative 123; Mismatches 196; Indels 11; Gaps 5;
QY 24 MRWILCWSLFLCMA--QFALGALHTKRPQVWTKYGLQCKQKHVGKTPIQVFLGVPSR 81
DB 3 LRSLFLVSLATCVGNGPSPVVDTKMGKVLKVASLEGVTSQVA-----VFLGVPPAK 57
QY 82 PPLGIIRFAPPEPEPKGIRDTATYPGCLQESW-GOLASVMVSTREYKWLRSDECL 140
DB 58 PPGSLRFPAPPAPAEPSFVNKTITTPPCSDATKGQVNDLLTNKKEKVLHQSEDC 117
QY 141 YLVNYPAPAPGDPQLPVMVWFFGGAFIVGAASVEGSDLAAREKVVFLVFLQRLGIFG 200
DB 118 YLVNIYPADFTKDSRNPVMVWIIHGGITQGGASTYDQVLSAVENVVVAIQVRLGIWGF 177
QY 201 LSTDDSHARGNGLLDQALRWQENIAAFGDPGNVTLFGOSAGAMISGLMMSPLAS 260
DB 178 FSTGDEHSRGNWGHLDQVAALHWQDNIAFNGDPSGVTFIFGESAGFSVSLVLSPLSK 237
QY 261 GLFHRAISQSGTALFRLFITSNPLKVAKVVAHLAGCNHNSSTOILVNLRLALSGTKMVRVS 320
DB 238 NLVHRAISEGVVLTFLTKDVRPAKQIADWAGCKTTSALIVHCLRQKTEBELLEIM 297
QY 321 NKVRFLQNFQRPDEIISMSVPWPGWIPDPVLLTQGVSSVYPVLLGVNVLFEFWL 380
DB 298 EKVNLIKLSQRDTKESYHFLSVLVDVLPKDPKEILAEKNFNTVPYIVGINKQBCGWL 357
QY 381 LPVIMKPLNQRAMKRTITKMLWSITLNLNITKEQVPLVVEYLDNVNEHMKWLNRM 440
DB 358 LPINRFPVDPVLDKQKQAMLEKFAISYIGIEDIIPVAIEKY--RKSGDDPIKIRDI 415
QY 441 MDIVQDATFYVATQTAHYHRDAGLPVLYVEFEHH--ARGIIVKPRDTGDHGDHMYFLRG 499
DB 416 LAFIGDVLFCIPSWVMSRDRDAGAPTYVYVYQYFSSPQRPKDVGVGDHADDVYVFG 475
QY 500 GPATGLSMCKEVALSLQMKYKVFANFARTGNPDGNLPCWPRYNKDEKYLQIDFTIRGM 559
DB 476 APILRDGASBEETKLSQMKVKFANFARNGNPNARGLPHPQPDYQKEEYLQIGATTQQSQ 535
QY 560 KLKEKKQMAFWNSLYQSQRPE 579
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DB 536 RLKAEVAFWTQLLAKRQPQ 555
RESULT 8
EST4 RAT STANDARD; PRT; 561 AA.
AC Q64573; Q62679;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Liver carboxylesterase 4 precursor (EC 3.1.1.1) (Carboxylesterase ES-4)
DE (Microsomal palmitoyl-CoA hydrolase) (Kidney microsomal
DE carboxylesterase) (Rat).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID:10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=96190723; PubMed=8611161;
RA Robbi M., van Schaftingen E., Beaufay H.;
RT "Cloning and sequencing of rat liver carboxylesterase ES-4
RT (microsomal palmitoyl-CoA hydrolase).";
RL Biochem. J. 313:821-826(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
RX MEDLINE=95050819; PubMed=7961958;
RA Van B., Yang D., Brady M., Parkinson A.;
RT "Rat kidney carboxylesterase. Cloning, sequencing, cellular
RT localization, and relationship to rat liver hydrolase.";
RL J. Biol. Chem. 269:29688-29696(1994).
CC -!- FUNCTION: INVOLVED IN THE DETOXIFICATION OF XENOBIOTICS AND IN THE
CC ACTIVATION OF ESTER AND AMIDE PRODRUGS. HYDROLYSES OMICRON-
CC NITROPHENYL ACETATE AND ALPHA-NAPHTHYL ACETATE. IT ALSO
CC HYDROLYZES ACETANILIDE AND, DISTINCTIVELY, PALMITOYL-COA.
CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a
CC carboxylic anion.
CC -!- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic
CC reticulum.
CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X81825; CAA57419.1; -.
DR EMBL; U10697; AAA64638.1; -.
DR PIR; S62788; S62788.
DR HSP; P21836; IMAA.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000886; ER_target_5.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;
KW Signal; Multigene family.
FT SIGNAL 1 18
FT CHAIN 19 561
FT ACT_SITE 221 221
FT ACT_SITE 466 466
FT DISULFID 87 116
FT DISULFID 273 284
FT SITE 558 561
FT CARBOHYD 79 79
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Matches	240;	Conservative	105;	Mismatches	191;	Indels	27;	Gaps	
Qy	26	WI	--LCW-SLTCIM--	AQTALGALHTKRPQVTKYTGLOGKQHVGTKIQTQVFLGVPFSS	80				
Dd	2	WLCALVWASLAVCP	IWHGPSSPPVDDTTKGVKGLKYSLEGFTQ----	FVAVFLGVGPPA	56				
Qy	81	RPLGLILRAPPEP	PEPPKGI	DATATYPPGCLOES--WGCLASMYVSTREYKWLRSDEC	139				
Dd	57	KPLGLSLRAPPEP	APPEP	PFVKNVTYTPMCSQGVKGLADMLSTGKESI	116				
Qy	140	LYNVYAPARAPCD	PQLP	PVVMFPGGAFIVGAASSYEGSDIAAREKVVVLVFLQHRIGIFG	199				
Dd	117	LYNIYSPADLT	KNSRLP	PVMWIHGGLIGGASPYSGLASAHENVVVTIQYRLGIWG	176				
Qy	200	FLSTDDSHARGNWGL	LDQMAALRWQENIAAF	GGDPGNVTLPFGOSAGAMSISGLMMSP	259				
Dd	177	LFTSGDEHGRGNW	ALDQLAALRWQDIANF	CGNPDSVTIFGSSAGVSVSALVLSPLA	236				
Qy	260	SGLFHRAISQS	GTAFLFR	LITSNPLKVAKKVAHLAGCNHNSTOILVNLCLRALSGTKVMRV	319				
Dd	237	KNLFHRAISES	GVLTNLDK	KNYQAVAQMIATISGCNTSSAAMVOC	287				
Qy	320	SNKRFPLQNFORD	PEEIIWNSPVVDGV	IPDPLVLTQGVSSYPYLLGVNNLEFNW	379				
Dd	288	KTEAELEL	TVLNDNT---	SMSTVIDGWLPKTPESILT	343				
Qy	380	LLPYIMKFFLN	RQAKETITK	WLSTLTLANITKEQVPLVVEYLDVNNHDKWMLNR	439				
Dd	344	IPTMGNLLSGR	NKWEKASFL	KRFPENLINESVIPAIIEKYLRGTDDPAKK--	401				
Qy	440	KMDIVODATFV	YATLQTAHYHRD	AGLPVLYEFEHFGHARGII--VKPRTDGADHGDEMYP	498				
Dd	402	LLDMPSDFV	FGIPAVLMSRSL	RADAGAPTYEFOYRPSFVSDQRPQIVQGDHGD	461				
Qy	499	GGPFATGLSMG	EKALSQMKYWAN	FARTGNPDGNLPCWPYRNKDEKYLQIDFTTRVG	558				
Dd	462	GTFFFLKEGAS	EEETNLSKLVMKFWAN	PNNGEGLHPWPKYDQKEGYLQIGATTQQA	521				
Qy	559	MKLKSKKAF	WMSLYQSORPEKQ	581					
Dd	522	QKLKEEVA	FWTELLAKNP	PQTE 544					
RESULT 10									
ESTN MOUSE									
ID	ESTN MOUSE	STANDARD;	PRT;	554 AA.					
AC	P23953;								
DT	01-VAR-1992	(Rel. 21, Created)							
DT	01-VAR-1992	(Rel. 21, Last sequence update)							
DT	28-FEB-2003	(Rel. 41, Last annotation update)							
DE	Liver carboxylesterase	precursor (EC 3.1.1.1)							
GN	ES1.	(PSS-N).							
OC	Mus musculus (Mouse).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
CC	NB_L1taxid=10090;								
RN	[1]								
RC	SEQUENCE FROM N.A.								
RP	STRAIN=C57BL/6J; TISSUE=Liver;								
RX	MEDLINE=911169540; PubMed=1840565;								
RA	Ovnic M., Tepperman K., Medda S., Elliott R.W., Stephenson D.A.,								
RA	Grant S.G., Ganschow R.E.;								
RT	"Characterization of a murine cDNA encoding a member of the								
RT	carboxylesterase multigene family."								
RL	Genomics 9:344-354(1991).								
CC	-!- FUNCTION: Involved in the detoxification of xenobiotics and in the								
CC	activation of ester and amide prodrugs.								
CC	-!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a								
CC	carboxylic anion.								
CC	-!- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic								
CC	reticulum.								
CC	-!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.								



DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;  
 FT SIGNAL 1 27  
 FT CHAIN 28 561  
 FT ACT\_SITE 227 227  
 FT ACT\_SITE 459 459  
 FT DISULFID 95 122  
 FT DISULFID 280 291  
 FT SITE 558 561  
 FT CARBOHYD 276 276  
 FT CARBOHYD 362 362  
 SQ SEQUENCE 561 AA; 62330 MW; 48EA1E42475321 CRC64;

Query Match 34.18; Score 1060; DB 1; Length 561;  
 Best Local Similarity 41.1%; Pred. No. 1.3e-76;  
 Matches 234; Conservative 97; Mismatches 191; Indels 48; Gaps 14;

Qy 29 CWSLTCLMAQTALGALH--TKRPQVTKYGLQGMHVV--GKTPIQVFLGVPSRPP 83  
 Db 8 CWRVAVACGLLLLVHVGQDSVSPINHTGQVRGLVYKGVGTGVVAFGLIPAKPP 67  
 Qy 84 LGILRFAPPPPPPKGIRATVPPGCLQESW--GQLASMYVSTRER---YKWLRFESD 138  
 Db 68 VGPLRFAPPPPPPPKSGVRDGTSEPAACLQTFMRPQI-----SKRKILFTISMSD 121  
 Qy 139 CLYLVNVPARAPGDPOLPVMMWFFPGGAFIVGASSVEGSDLAAREKVLVLFQHLGIF 198  
 Db 122 CLYLVNITPAHAGSNLPVMMWTHGALVNGASNMDSLLAATEDIVIVSYQYRLGIL 181  
 Qy 199 GFUTDSDHARGNWGLLDQMAALRWQENIAAAGGDPGNVTLFGQSAGAMISGLMMSP 258  
 Db 182 GFSTGDEHARGNWGLDQVAALHWQONIASFGNGPQVTIFGSAAGTSVSLVSPM 241  
 Qy 259 ASGLFHRAISQSTALFRLTISNELKV-AKVAHLAGCNHNSQILVNCRLALSGTKVM 317  
 Db 242 SKGLFHRAIQSGVALPDLISDTPEAVYTPVWANGSGCEAKSEALVHCLREKTEAEIL 301  
 Qy 318 RVSNMRLQLNFORDEPEEIIWNSP--VVDGVVIPPDPPLVLLAQGVSSVPYLLGVNNE 376  
 Db 302 AINQ-----VFINTPGVDGIFLRHPQELLASVDVFPVPSIIGVDSDE 345  
 Qy 377 FNWLLPYMKFPLNQMRKETTQKMLWSTRLTNITKEQVPLVVEYLDNVNEHWKML 436  
 Db 346 CGMGVPLFGLDHYVKNITRETLPAFLKSRAEHMLPPECSDLMLQYMGDV--EDPQL 403  
 Qy 437 RNRNMDIVQDATFYVATQTAHYHRDAGLPVLYEPEHARGI---IVKPRTDGADHDE 493  
 Db 404 QAQFEELMKDFMFIPLKAVYQYR-SHAPVYFEFOHQSSFIKNKDARPSHVRADGHD 462  
 Qy 494 MYELFGPPFATGLSMG---KEKALSQMKYKWNANFARTGNPDGNLPCWPRYKNKDEKYLQ 550  
 Db 463 VAFVFGSDF-WGLKIDLTBEKLLNKRMKYKWNANFARHGNPNSEGLPYNPDELVHDDQYLK 521  
 Qy 551 LDFTRVGMKLEKKVAFWMSLYQSQRPEK 580  
 Db 522 LDIQPAVGRAKSKLHFHWKIL-----PQK 547

RESULT 13

ESTM\_MOUSE

ID\_ESTM\_MOUSE

AC\_Q63880;

DT\_01-NOV-1997 (Rel. 35, Created)

DT\_01-NOV-1997 (Rel. 35, Last sequence update)

DT\_28-FEB-2003 (Rel. 41, Last annotation update)

DE\_Liver carboxylesterase precursor (EC 3.1.1.1)

GN\_E831.

OS\_Mus musculus (Mouse)

OC\_Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC\_Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX\_NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX STRAIN=BAJB/CJ X DBA/2J; TISSUE=Liver;  
 RX MEDLINE=93326638; PubMed=7916639;  
 RA Aida K., Moore R., Negishi M.;  
 RT "Cloning and nucleotide sequence of a novel, male-predominant  
 RT carboxylesterase in mouse liver";  
 RL Biochim. Biophys. Acta 1174:72-74 (1993).  
 CC -!- FUNCTION: Involved in the detoxification of xenobiotics and in the  
 CC activation of ester and amide prodrugs.  
 CC -!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a  
 CC carboxylic anion.  
 CC -!- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic  
 CC reticulum.  
 CC -!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
 CC  
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 CC -----  
 CC EMBL; S64130; AAB27606.1; -;  
 DR PIR; S34607; S34607.  
 DR HSSP; P37967; 1QB3.  
 DR MGD; MGI:102773; Es31.  
 DR InterPro; IPR002018; Carboxylesterase.  
 DR InterPro; IPR000379; Ser. esters.  
 DR Pfam; PF00135; Coesterase; 1.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;  
 FT SIGNAL 1 14  
 FT CHAIN 15 554  
 FT ACT\_SITE 215 215  
 FT ACT\_SITE 443 443  
 FT DISULFID 83 110  
 FT DISULFID 267 278  
 FT SITE 551 554  
 FT CARBOHYD 294 294  
 FT CARBOHYD 300 300  
 FT CARBOHYD 381 381  
 SQ SEQUENCE 554 AA; 61509 MW; 028D98B06F3CAAD CRC64;

Query Match 33.2%; Score 1034; DB 1; Length 554;  
 Best Local Similarity 41.1%; Pred. No. 1.3e-74;  
 Matches 232; Conservative 89; Mismatches 205; Indels 38; Gaps 9;

Qy 34 LCLMAQTALGALHTKRPQVTKYGLQGMHVGKTP--IQVFLGVPSRPPGLILRPAP 91  
 Db 5 LLIFPTTVIGPKVT-QPEVDTPLGVRGRQGVKDTDRMVMVFLGIPPAQAPGLRPSA 63  
 Qy 92 PEPPEPWKIGIRDATYPPGCLQESWGQLASVMVSTREYKWLRFESDCLYLVNVPARAP 151  
 Db 64 PLFPQFQWEGVRDASINPPMCLQDV-ERMNSRFTLINEKQKIFPISDCLTNLYSPTEIT 122  
 Qy 152 GDPQLPVNMWFFPGGAFIVGAASVEGSDLAAREKVLVFLQHLGIFGLSTDSDHARGN 211  
 Db 123 AGDKRPVMMWTHGSLRVSGSSTSHDGSALAAGVGVVVTVQYRLGIFGLSTGDKHMPGN 182  
 Qy 212 WGLLDQMAALRWQENIAAAGGDPGNVTLFGQSAGAMISGLMMSPASGLFHRAISQSG 271  
 Db 183 RGFLDVAALRWQENIAPFGGDPNCVTFIAGNSAGGIIVSSLLSPMSAGLPHRAISQSG 242  
 Qy 272 TALFRLFITSPKLVAKVAHLAGCNHNSQILVNCRLALSGTKVMRVSNNMRLQLNLFQ 331  
 Db 243 VVISKILSDLNWSEAFQNFANSVACGSAPAEVLQCLLQKEGKDLITKKNV----- 293  
 Qy 332 RDPSEIIVMSPPVDGVVIPPDLVLLFQGVKSSVPYLLGVNNEFWNLLPYIMKFPPLNR 391  
 Db 294 -----NISYTVNDSFFPQPKLANKQFPTVYLLGVNTHFEFGWLL---LKFWNIL 342



QY	392	QAMRKETITKMLSTRLL--NITKEQVPLVVEEYLDNNEHDMKMLRNMDIVQDAT	448
Db	343	DKVEHLSQEDLLENSRELLAHMQLPPEIMPTVIDEYLDNGS--DESATRYAQELLGDT	400
QY	449	FVYATLQTHYHRDAGLPVLYFEHARGII-VKPRTDGADHGDHMYFLFGPPFATGUS	507
Db	401	LVIPTLIFSXYLDAGCPVLYEFQHTPSSFAKPKPAWKADHSSSENAFVFGPFLTDES	460
QY	508	-----MCKEKALSLQMKYKYNANPARTGNPDGNLPCWPRYKDKYQLDFTTRVGM	559
Db	461	SLAAPPATEEELKSLUTMAQNSQFARTGNPKGLPPWQNLQLEIGLEPRTGV	520
QY	560	KLKEKMAFWMSLYSQSRPEKQRQ	583
Db	521	KLKKGRLQFWTETLPKRIQEWRE	544
RESULT 14			
EST2	RABIT	STANDARD;	PRT; 532 AA.
AC	P14943;		
DT	01-APR-1990 (Rel. 14, Created)		
DT	01-FEB-1994 (Rel. 28, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Liver carboxylesterase 2 (EC 3.1.1.1).		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9586;		
RN	[1]		
RP	SEQUENCE.		
RC	TISSUE=Liver;		
RX	MEDLINE=89308686; PubMed=2745458;		
RA	Ozols J.;		
RT	"Isolation, properties, and the complete amino acid sequence of a		
RT	second form of 60-kDa glycoprotein esterase. Orientation of the		
RT	60-kDa proteins in the microsomal membrane."		
RL	J. Biol. Chem. 264.12333-12345(1989).		
CC	-!- FUNCTION: Involved in the detoxification of xenobiotics and in the		
CC	activation of ester and amide prodrugs.		
CC	-!- CATALYTIC ACTIVITY: A carboxylic ester + H(2)O = an alcohol + a		
CC	carboxylic anion.		
CC	-!- SUBUNIT: Monomer.		
CC	-!- SUBCELLULAR LOCATION: Microsomal membrane, lumen of endoplasmic		
CC	reticulum.		
CC	-!- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.		
DR	PIR; A34329; A34329.		
DR	HSSP; P37967; 1QE3.		
DR	InterPro; IPR002018; CarbesteraseB.		
DR	InterPro; IPR000379; Ser esters.		
DR	Pfam; PF00135; Coesterase_1.		
DR	PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.		
DR	PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.		
KW	Glycoprotein; Hydrolase; Serine esterase; Endoplasmic reticulum;		
KW	Pyrolidone carboxylic acid.		
FT	MOD_RES	1	PYROLIDONE CARBOXYLIC ACID.
FT	ACT_SITE	201	BY SIMILARITY.
FT	ACT_SITE	430	BY SIMILARITY.
FT	DISULFID	69	BY SIMILARITY.
FT	DISULFID	253	BY SIMILARITY.
FT	SITE	529	PREVENT SECRETION FROM ER (POTENTIAL).
FT	CARBOHYD	249	N-LINKED (GLCNAC...).
SQ	SEQUENCE	532 AA;	5905 MW; C57DD76A13A9C52 CRC64;
Query Match			
Best Local Similarity 31.98; Score 993; DB 1; Length 532;			
Matches 226; Conservative 85; Mismatches 162; Indels 72; Gaps 15;			
QY	54	TKYTGKQKMHVGKTP--IQVFLGVFSPPLGILRFAPEPPKGIKRDATTYPGCG	111
Db	10	THTQVQSGSLVHVEGTGAGVHTFLGIPFAKPLGLPLRFAPEPAEAWSGVRDGTSLPAMC	69

QY	112	LQESWGOLASMYSTRERYKWLRF-----SBDCLYVNYAPARAPGDPQLPVMWVFP	164
Db	70	LQ-----NLAIM-----DQVILLHFTPPSIPIWSEDCLYINITYSAHAREGSDLPVWVIHG	121
QY	165	CATVGAASSVEGSDLAAREKVLVFLQHLRGLFGFLSTDDSHARGNWGLDQMAALRW	224
Db	122	GGLTNGVASMVDGSAALAEEDVVVVITQYRLVGLGFFSTGQHQATGNHGYLDQVAALRW	181
QY	225	QENIAAFGGPGNVTLFGQAGAMSIISLMMSPSLASGLPHRAISQSGTALFLRITSNPL	284
Db	182	QKNIAHFGGNPGRVTIFGESAGGTSVSSHVLSPMWQGLPHGAIMESLVALPLGLITSSE	241
QY	285	KVAKYVAHLACNNHSTQILVNCILRALSCTKWEVSNQWFLQLNFORDEEIIWNSPV	344
Db	242	VSTVANLGRCGQVDSETLVRCLRAKSEBEMLAIT-----QVFMIFGV	286
QY	345	VDGVVIPDDPLVLLTQGVSVSPVYLLGVNNLEFNWLLPYIM-----KFPNLRQMRK--E	397
Db	287	VDGVFLPRHPPELLALADFPVPSIIGINNDEYGVIIIPKLLAIDPQEDRDQAMREIMH	346
QY	398	TITKMLSTRTLNITKEQVPLVVEEYLDNNEHDMKMLRNMDIVQDATFYATLQTA	457
Db	347	QATKQLMLPPALGD-----LLMDEYMGs-NE-DPKHMAQFQEMMADAMFYMPALRVA	397
QY	458	HYHRDAGLPVLYFEH-----HARGIIVKPTDGDHGDHMYFLFGGP-FATG	505
Db	398	HLQR-SHAPTYFYEFQHRPSFTKDLRPPHYR-----ADHGDEVVVFVRSFLFGSK	446
QY	506	LSM-GKSKALSLQMKYKYNANPARTGNPDGNLPCWPRYKDKYQLDFTTRVGMKLEK	564
Db	447	VPLTEEBELLSRRVMKYKYNANFARNRNPNGEGLAHWPLFDLDQRYLQNMQPAVGQALKAR	506
QY	565	KMAFW 569	
Db	507	RLQFW 511	
RESULT 15			
NLG2	RAT	STANDARD;	PRT; 836 AA.
AC	Q62888;		
DT	10-OCT-2003 (Rel. 42, Created)		
DT	10-OCT-2003 (Rel. 42, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Neurologin 2 precursor.		
GN	NLGN2.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), SEQUENCE OF N-TERMINUS, TISSUE		
RP	SPECIFICITY, AND INTERACTION WITH NEUREXIN 1-BETA; NEUREXIN 2-BETA AND		
RP	NEUREXIN 3-BETA.		
RC	TISSUE=Forebrain;		
RX	MEDLINE=96162010; PubMed=8576240;		
RA	Ichchenko K., Nguyen T., Suedhof T.C.;		
RT	"Structures, alternative splicing, and neuroligin binding of multiple		
RT	neurologins."		
RL	J. Biol. Chem. 271:2676-2682(1996).		
RN	[2]		
RP	TISSUE SPECIFICITY.		
RX	MEDLINE=21226491; PubMed=11329178;		
RA	Gilbert M., Smith J., Koskams A.J., Auld V.J.;		
RT	"Neurologin 3 is a vertebrate gliotactin expressed in the olfactory		
RT	ensheathing glia, a growth-promoting class of macroglia."		
RL	Glia 34:151-164(2001).		
CC	-!- FUNCTION: Neuronal cell surface protein thought to be involved in		
CC	cell-cell-interactions by forming intercellular junctions through		
CC	binding to beta-neurexins. Seems to play role in formation or		
CC	maintenance of synaptic junctions. In vitro, triggers the de novo		
CC	formation of presynaptic structures (By similarity).		
CC	-!- SUBUNIT: Interacts with neuroligin 1-beta isoforms 3/Beta 4B5A and		



```
CC 4/Beta 4B5B. Interacts with neuroligin 2-beta isoforms 3/Beta 4B5A,  
CC 4/Beta 4B5B, 7/Beta 4B5A6 and 8/Beta 4B5B6. Interacts with  
CC neuroligin 3-beta. Probably interacts through its C-terminus with  
CC DLG4/PSD-95 third PDZ domain (By similarity).  
CC -|- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
CC -|- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q62888-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q62888-2; Sequence=VSP_007533;  
CC -|- TISSUE SPECIFICITY: Expressed in brain, spinal chord and dorsal  
CC root ganglion.  
CC -|- SIMILARITY: Belongs to the type-B carboxylesterase/lipase family.  
CC  
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CC  
CC EMBL; U41662; AAA97870.1; -;  
CC HSP; P37967; IQE3.  
CC InterPro; IPR002018; CarboxylesteraseB.  
CC InterPro; IPR000460; Neuroligin.  
CC InterPro; IPR000379; Ser_estrs.  
CC Pfam; PF00135; Coesterase; 1.  
CC PRINTS; PS01090; NEUROLIGIN.  
CC PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.  
CC Cell adhesion; Glycoprotein; Signal; Transmembrane;  
KW Alternative splicing  
FT SIGNAL 1 PROBABILE.  
FT CHAIN 15 836 NEUROLIGIN 2.  
FT DOMAIN 15 678 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 679 699 POTENTIAL.  
FT DOMAIN 700 836 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 106 141 BY SIMILARITY.  
FT DISULFID 317 328 BY SIMILARITY.  
FT DISULFID 487 521 BY SIMILARITY.  
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPLIC 153 169 Missing (in isoform 2).  
FT FTId=VSP_007533.  
SQ SEQUENCE 836 AA; 90961 MW; 1AD51CB1BE4BF9CF CRC64;  
  
Query Match 27.3%; Score 849; DB 1; Length 836;  
Best Local Similarity 33.2%; Pred. No. 1.3e-59;  
Matches 215; Conservative 92; Mismatches 191; Indels 150; Gaps 21;  
  
Qy 30 WSLTLCLM-----AQ-----TALGALHTKR-PQVVTKYGTLOGQMVGKT 69  
Db 2 WLLALCLVLGAGQGGGPGGAPGGGLGLGLEERFPVNVTAIVRGVRRLEANE 61  
  
Qy 70 ---PIQVFLGVFSPPLGILRFAPPEPPFPKGIKIDATTPPGCLQESWGOL----- 119  
Db 62 ILGPVVQVLGVVATPPLGARRRFPQPEAPASWFGVNRATTLPPACPNLHGLPAIMLPV 121  
  
Qy 120 -----ASMVSTRERYKWLRFESDCLVINYAPAR-----APGDPQL-- 156  
Db 122 WFTDNLLEAAATYVQNG-----SEDCLYNLNVPTEDGPLTKKDEATLNPDPDIRD 173  
  
Qy 157 ---PVNVWFPFGGAFIVGAASSYEGSDLAAREKVLVFLQHRIGIFGLSTDDSHARGNW 212  
Db 174 SGKKPVMFLHGGSYMEGTGMVFDGSLAAYGNVIVATLNYRLGVLFSTGDAQAKGY 233  
  
Qy 213 GLLDQVAALRWQENIAAFGGDPGNVTFLFQGSAGAMISGLMMSPLASGLFHRATISQSGT 272  
Db 234 GLLDQIQALRWLSENIAHFQGDPERITIFGSGAGASCVNLLILSHSEGLFQKATQSGT 293  
  
Qy 273 ALFRLFTITSNPLKVAKVHLAGCNHNSITQLVNCRLALSGTKVMVSNKMRFLQLNFOR 332
```

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Db 294 AISSWSVNYQPLKYTRLLAAKVGCDREDSTEAVECLRRKSSREL-----VDQDV 342  
Qy 333 DPBEELIWSMSPVGVGWIIPDDPLVLLTQGGKVSVPYLLGVNNLB----- 376  
Db 343 QPARYHIAFGPVVDGVDVDDPEILMQGGEFLNVDMLIGVNOGGLKFEVDSAESEGV 402  
Qy 377 ---FNW-----LLPYIMKFPPLNRQARMKETITKMLWSTRLTLNITKEQVPLVVEYLDNVN 429  
Db 403 ASAFDFTVSNEVDNLYGYPEGKDLR-ETIKFM-----YTDWAD 440  
Qy 430 EHDKMLNRMMDIVQDATFVYATLQTAHVHRDAGLPVLYEPEHH--ARGIIVKPRTDG 487  
Db 441 RDNGEMRKTLTLLTTHQWVAPATAKLHADYQSPYFTTFYHHQAEQ---RPEWAD 497  
Qy 488 ADHGDMEYLFEGGPF--ATGL---SMGK-EKALSLOMKYKAWANFARTGNPNDGNLP--- 537  
Db 498 AAHGDELPPYVFGVPMVGATDLFPCNFSKNDVMSLAAVVMYWTNFAKTGDPNQ-PVPQDTK 556  
Qy 538 -----CWPRYN-KDEKYLQDLFTTRVGKMLKEKKMAFMMSL 572  
Db 557 FIHTKPNRFEVWWSKFSKSKQYLHGLKPRVRDNRANKVAFWLEL 604
```

Search completed: August 3, 2004, 22:28:20

Job time : 15 secs



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OM protein - protein search, using sw model

Run on: August 3, 2004, 22:24:10 ; Search time 42 Seconds

(without alignments)  
4387.205 Million cell updates/sec

Title: US-10-001-227-2

Perfect score: 3112

Sequence: 1 MPSTVLPSTVLSPLPTAGA.....KMAFWNLSVQSRPEKQRF 584

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriopl.\*
- 17: sp\_archaea.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2182.5	70.1	556	11 Q8R0W5	Q8R0W5 mus musculus
2	1930	62.0	367	4 Q8N9F4	Q8N9F4 homo sapien
3	1287.5	41.4	556	6 Q864S9	Q864S9 felis silve
4	1284	41.3	555	6 Q95N05	Q95N05 canis famil
5	1282	41.2	556	6 O46421	O46421 macaca fasc
6	1265	40.6	555	4 Q96EE8	Q96EE8 homo sapien
7	1264	40.6	555	4 Q8T0Z9	Q8T0Z9 homo sapien
8	1260	40.5	555	6 O77540	O77540 corytolagus
9	1254	40.3	555	11 Q9R135	Q9R135 rattus norv
10	1252	40.2	555	11 Q91YG2	Q91YG2 rattus norv
11	1248.5	40.1	557	4 Q9UK77	Q9UK77 homo sapien
12	1247	40.1	555	11 Q35534	Q35534 mesocricetu
13	1244.5	40.0	555	11 Q91ZV9	Q91ZV9 mus musculu
14	1244.5	40.0	555	11 Q8VCT4	Q8VCT4 mus musculu
15	1242.5	39.9	555	11 Q924V8	Q924V8 mus musculu
16	1241	39.9	555	6 O97582	O97582 sus scrofa

17	1239	39.8	567	4 Q86UK2	Q86UK2 homo sapien
18	1235.5	39.4	567	4 Q8ULY1	Q8ULY1 homo sapien
19	1198.5	38.5	565	11 Q8VCC2	Q8VCC2 mus musculu
20	1196.5	38.4	565	11 Q55136	Q55136 mus musculu
21	1155	37.1	545	6 Q81034	Q81034 felis silve
22	1145.5	36.8	561	11 Q91WU0	Q91WU0 mus musculu
23	1140	36.6	565	11 P70104	P70104 cavia porce
24	1130.5	36.3	554	11 Q54936	Q54936 mus musculu
25	1130.5	36.3	554	11 Q8K125	Q8K125 mus musculu
26	1122	36.1	559	11 Q35533	Q35533 mesocricetu
27	1116	35.9	562	11 Q924V9	Q924V9 rattus norv
28	1100	35.3	560	11 Q8R097	Q8R097 mus musculu
29	1083	34.8	559	4 Q00748	Q00748 homo sapien
30	1083	34.8	623	4 Q81UP4	Q81UP4 homo sapien
31	1079.5	34.7	561	11 Q70177	Q70177 rattus norv
32	1068	34.3	554	11 Q35535	Q35535 rattus norv
33	1067.5	34.3	568	4 Q72601	Q72601 homo sapien
34	1063	34.2	572	11 Q810S9	Q810S9 mus musculu
35	1058.5	34.0	558	11 Q8K3R0	Q8K3R0 rattus norv
36	1057	34.0	559	11 Q8BK48	Q8BK48 mus musculu
37	1053.5	33.9	558	11 Q8Q2R3	Q8Q2R3 mus musculu
38	1053.5	33.9	561	11 Q91WGO	Q91WGO mus musculu
39	1051.5	33.8	568	11 Q8VCU1	Q8VCU1 mus musculu
40	1047	33.6	559	11 Q8BN97	Q8BN97 mus musculu
41	1045	33.6	607	4 Q8T0P8	Q8T0P8 homo sapien
42	1044	33.5	607	4 Q7Z366	Q7Z366 homo sapien
43	1024	32.9	525	4 Q96DN9	Q96DN9 homo sapien
44	1021.5	32.8	561	11 Q70631	Q70631 rattus norv
45	956	30.7	469	4 Q8NBC8	Q8NBC8 homo sapien

#### ALIGNMENTS

#### RESULT 1

Q8R0W5 PRELIMINARY; PRT; 556 AA.

AC Q8R0W5; 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS BC026374.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RA Strausberg R.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.

DR EMBL; BC026374; AAH26374.1; -.

DR MGI; MGI:2384581; BC026374.

DR GO; GO:0016787; F:hydrolase activity; IEA.

DR InterPro; IPR002018; CarboxylesteraseB.

DR InterPro; IPR000379; Ser\_estrs.

DR Pfam; PF00135; Coesterase; 1.

DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.

DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.

KW Hypothetical protein; Hydrolase.

SQ SEQUENCE 556 AA; 62122 MW; EB31F4F34990446 CRC64;

Query Match 70.1%; Score 2182.5; DB 11; Length 556;

Best Local Similarity 71.8%; Pred. No. 5.5e-177;

Matches 400; Conservative 68; Mismatches 86; Indels 3; Gaps 3;

QY 24 NRWICWLSLTCLMAQTALGALHTKRPVVTKYGTLOGKQHWGKTPIQVFLGVFFSRPP 83

1 MKWILGLSLTCLVQVQALGALHTKEPLITKHILOGKQVHVGDTPIQVFLGIFPSKPP 60

QY 84 LGILRFAPPEPPEPWKIGIRDATTTPGCLQBSWQLASMYVSTRERYKNLWRFSEDCLYLN 143

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Db      61  VGTERRAPPBPPIPWNGIRDATTPSCLOESWGQILSMYLNTRKQYKWLHSESDCLYN 120
QY      144  VYAPARAPGDPQPLVPMWPPFGGAFIVGAASSYEGSDLAAREKVLVFLQHRIGIFGFLST 203
Db      121  VYAPVLAPGAPLPLVPMWPPFGGAFIVGAASSYEGSDLAAREKVLVFLQHRIGIFGFLST 180
QY      204  DSHARGNWLGLDQMAALRWQENIAAFGDPGNVTLFGOSAGAMISGLMSPPLASGLP 263
Db      181  GNSHARGNWLGLDQMAALRWQENIAAFGDPGNVTLFGOSAGAMISGLMSPPLASGLP 240
QY      264  HRAISOGTALFLFTITSNPLKVAHLAGNCHNSTOILVNCRLALSGTKVMRVSNM 323
Db      241  HQAISOGTAVLKAFITPPLTSKAKIAHLAGNCHNSTOILVNCRLALSGTKVMRVSNM 300
QY      324  RELQNFQRPDPEIISWSPVVDGVPVDDPLVLLTQGVSSVYLLGVNNEERWLLPY 383
Db      301  SFTQASHKDPKEIVFLSPVVDGVPVDDPLVLLTQGVSSVYLLGVNNEERWLLPY 360
QY      384  IMKFPNLRQARKEITIKMLWSTRTLLNITKEQVPLVVEEYL-DNVNEDHDKMLNRMD 442
Db      361  LMKIQLNORMWNTNINKILWSPVVDGVPVDDPLVLLTQGVSSVYLLGVNNEERWLLPY 420
QY      443  IVODATFVYATQATYHRDAGIPVLYEFHHA-RGIIVKPTDGDHGDGDEMIFLFGP 501
Db      421  LIGDATFVYATQATYHRDAGIPVLYEFHHA-RGIIVKPTDGDHGDGDEMIFLFGP 479
QY      502  FATGLSMGKEKALSQVMKWYANFARTGNPNCNLPWRYNKDEKYLQDFTTRVGMKL 561
Db      480  FSKGSAGKEKALSQVMKWYANFARTGNPNCNLPWRYNKDEKYLQDFTTRVGMKL 539
QY      562  KEKMAFWMSLYOSQRP 578
Db      540  KEKMAFWMSLYOSQRP 556

RESULT 2
Q8N9F4 PRELIMINARY; PRT; 367 AA.
AC Q8N9F4;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DE Hypothetical protein FLJ37464.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Oka T., Wakamatsu A., Ishii S.,
RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kikuchi H., Yamashita H., Matsuo K., Nakamura Y., Sekine K.,
RA Takahashi-Fujii A., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
RA Sugano S., Nagahari K., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA "NEDO human cDNA sequencing project."
RT Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AK094783; BAC04422.1;
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR Hypothetical protein; Hydrolase.
SQ SEQUENCE 367 AA; 41851 MW; 95671668E6F2FA7C CRC64;

Query Match 62.0%; Score 1930; DB 4; Length 367;
Best Local Similarity 99.7%; Pred. No. 9.3e-156;

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Matches 366; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY      218  MAALRWQENIAAFGDPGNVTLFGOSAGAMISGLMSPPLASGLPHRAISOGTALFRL 277
Db      1  MAALRWQENIAAFGDPGNVTLFGOSAGAMISGLMSPPLASGLPHRAISOGTALFRL 60
QY      278  FITSNPLKVAHLAGNCHNSTOILVNCRLALSGTKVMRVSNMKRFQLQNFQRPDPEI 337
Db      61  FITSNPLKVAHLAGNCHNSTOILVNCRLALSGTKVMRVSNMKRFQLQNFQRPDPEI 120
QY      338  IWSMSPVVDGVPVDDPLVLLTQGVSSVYLLGVNNEERWLLPYIMKFPNLRQARKE 397
Db      121  IWSMSPVVDGVPVDDPLVLLTQGVSSVYLLGVNNEERWLLPYIMKFPNLRQARKE 180
QY      398  TITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEDHDKMLNRMDIVQDATFYATLQTA 457
Db      181  TITKMLWSTRTLLNITKEQVPLVVEEYLDNVNEDHDKMLNRMDIVQDATFYATLQTA 240
QY      458  HYHRDAGLPVLYEFHHA-RGIIVKPTDGDHGDGDEMIFLFGPFGATGLSMGKEKALSQ 517
Db      241  HYHRDAGLPVLYEFHHA-RGIIVKPTDGDHGDGDEMIFLFGPFGATGLSMGKEKALSQ 300
QY      518  MMKWYANFARTGNPNCNLPWRYNKDEKYLQDFTTRVGMKLKEKMAFWMSLYOSOR 577
Db      301  MMKWYANFARTGNPNCNLPWRYNKDEKYLQDFTTRVGMKLKEKMAFWMSLYOSOR 360
QY      578  PEKORQF 584
Db      361  PEKORQF 367

RESULT 3
Q864S9 PRELIMINARY; PRT; 566 AA.
AC Q864S9;
DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Carboxylesterase.
GN CCSI.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Miyazaki M., Sai H., Taira H., Yamashita T.;
RT "Molecular cloning of the feline liver carboxylesterase."
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB094147; BAC75712.1;
DR GO; GO:0003824; F:catalytic activity; IEA.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
SQ SEQUENCE 566 AA; 62231 MW; 4677D3F67205AD53 CRC64;

Query Match 41.4%; Score 1287.5; DB 6; Length 566;
Best Local Similarity 45.7%; Pred. No. 9.6e-101;
Matches 252; Conservative 107; Mismatches 184; Indels 9; Gaps 6;
QY      26  WILCWSLTLCLMAQTALGALHTKRPQV-TKYGTLGKQMHV--KTQVFLGVFPSPR 82
Db      2  WLLALVLTSLTTSMTWAG--HPSSPPVDTSQKVLGXHVSGFAQPVAVLGIFFARP 59
QY      83  PLGILRAPPEPPEPWKIGIRDATTYPGCLQE-SMQLASMYVSTRERYKWLRFSEDCLY 141
Db      60  PLGSLRAPPEPPEPWKIGIRDATTYPGCLQE-SMQLASMYVSTRERYKWLRFSEDCLY 119
QY      142  LNVYAPARAPGDPQPLVPMWPPFGGAFIVGAASSYEGSDLAAREKVLVFLQHRIGIFGL 201

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Db 120 LNIYTPVDLRKKURLPVMVWIHGGGLMVGASTYSGVLVAHENVVVVVTIQYRLGIWGYF 179
Qy 202 STDSHARGWGLDDQAAALRWQENIAAFGGDPGNVTLFGOSAGAMSISGLMSPLAGS 261
Db 180 STDEHSRGNWGLDDQAAALRWQENIAFNGGPGSVTIIFGSAGGISVILVLSPLAKN 239
Qy 262 LFHRAISQSQTALFRIFITSNPLKVAKKVAHLACNNHSTQILVNCRLALSGTKVMRVSN 321
Db 240 LFHRAISGSVALITLVKKDKMDAAQQAIAFFAGCKNTTSAVTVCLRQKTEBEELEISR 299
Qy 322 KRFPLQINQRPDEEIIWMSPPVVDGVPDDPLVLLTGCKVSSVPYLLGVNLFBNWLL 381
Db 300 KMKFFTDIDYGSRENHAFPIVVDGVLFPKMPPEILAEKXFNFPVYIIGINKHFEGCL 359
Qy 382 PYIMKPLNRQMRKETTITKMLWSTRLNITKEOVPLVVEEVLNVDNHEHDKMLNRNM 441
Db 360 PKLMGVPLESEGLDQKTMASLLWKSPIIGIPEELIPLAEKYLEGTDDEPVKK--KDLFL 417
Qy 442 DIVQDATFVATLOTAYHRDAGLPVLYEFEHH-ARGIIVKPRTDGADHDEMFLFEG 500
Db 418 EVLGDAMFGVPSVTVARHHRDAGAPTYMVEFQVHPFSFSDMKPKTLIGDHGDELYSVFGA 477
Qy 501 PFATGLSMGKEKALS-QMKMYANFARTGNPDGNLPCWPRYNKDEKYLQDFTTRVGWK 560
Db 478 PFLKGSASEEIRLSKMMKFWANFARSGNPNEGGLPSWPAYDQKEGYLQIGATTQPAOK 537
Qy 561 LKEKMAFWMSL 572
Db 538 LKDKVAFWTEL 549

RESULT 4
Q95N05 PRELIMINARY; PRT; 565 AA.
AC Q95N05;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Carboxylesterase D1.
GN CESDD1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21237951; PubMed=11339814;
RA Hosokawa M., Suzuki K., Takahashi D., Mori M., Satoh T., Chiba K.;
RT "Purification, Molecular Cloning, and Functional Expression of Dog
RT Liver Microsomal acyl-CoA Hydrolase: A Member of the Carboxylesterase
RT Multigene Family,"
RL Arch. Biochem. Biophys. 389:245-253(2001).
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AB023629; BAB60696.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000379; Ser_estr.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 565 AA; 62000 MW; 905AA4222DEFD37B CRC64;

Query Match 41.3%; Score 1284; DB 6; Length 565;
Best Local Similarity 45.3%; Pred. No. 1.9e-100;
Matches 253; Conservative 106; Mismatches 192; Indels 8; Gaps 5;

Qy 26 WILCWSLTLCLMAQTALGALHTRPQVTKYGTLOGKQMHVG--KTFIQVFLGVPPSRPP 83
Db 2 WL--FDLVLTSLATSNAGVPSLPVVDVTQGVKLVYSLEGAQFVAVFLGVPPAKPP 59
Qy 84 LGILRFAPPPPPWKGIRDATTYPGCCLOES-WGQLASMYSTRYKWLRFSEDCLYL 142

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Db 60 LGPLRFAPPQAAEPWNEFVXNTTSYPPMCSQDAVGQVLSLFTNRKDNIPLKFSSEDCLYL 119
Qy 143 NVYAPAPAGDPQPLPVMVWPGGAFIVGAASSYEGSLAAREKVVLVFLQHLGIFGLS 202
Db 120 NIYTPADLTNRSLPVMVWIHGGGLVVGASTYDGLALSAHENVVVVVTIQYRLGIWGYF 179
Qy 203 TDDSHARGWGLDDQAAALRWQENIAAFGGDPGNVTLFGOSAGAMSISGLMSPLAGS 262
Db 180 TGDEHGRGNWGLDDQAAALRWQENIAFNGGPGSVTIIFGSAGGESVVLVLSPLAKN 239
Qy 263 FHRAISQSQTALFRIFITSNPLKVAKKVAHLACNNHSTQILVNCRLALSGTKVMRVSN 322
Db 240 FHRAISGSVALITLVKKDKMDAAQQAIAFFAGCKNTTSAVTVCLRQKTEBEELEVSLK 299
Qy 323 MRFLQLNFORPDEEIIWMSPPVVDGVPDDPLVLLTGCKVSSVPYLLGVNLFBNWLL 382
Db 300 LKFTLIDLFDPRESYFPLTVVDGVLFPKMPPEILAEKXFNFPVYIIGINKHFEGWLLP 359
Qy 383 YIMKPLNRQMRKETTITKMLWSTRLNITKEOVPLVVEEVLNVDNHEHDKMLNRNM 442
Db 360 MMGYPLSEDKLDQKTASLLWKSYPITANIPEELTPLAASEKYLGGTDDPVKK--KALFLD 417
Qy 443 IVQDATFVATLOTAYHRDAGLPVLYEFEHH-ARGIIVKPRTDGADHDEMFLFEGP 501
Db 418 MGDVVFQVPSVTVARHHRDAGAPTYMVEFQVHPFSFSDMKPKTVVGDHGDLESVFGAP 477
Qy 502 FATGLSMGKEKALS-QMKMYANFARTGNPDGNLPCWPRYNKDEKYLQDFTTRVGWK 561
Db 478 FLKGSASEEIRLSKMMKFWANFARSGNPNEGGLPSWPAYDQKEGYLQIGATTQPAOK 537
Qy 562 KEKMAFWMSLYQSRPEK 580
Db 538 KSKMAFWTELLAKRAAEK 556

RESULT 5
Q46421 PRELIMINARY; PRT; 566 AA.
ID Q46421
AC Q46421;
DT 01-JUN-1998 (T-EMBLrel. 06, Created)
DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Carboxylesterase precursor (EC 3.1.1.1).
OC Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver.
RA Sone T., Takabatake E., Isobe M.;
RT "cDNA cloning and characterization of a monkey liver
RT carboxylesterase,"
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AB010633; BAA24523.1; -.
DR HSP; P21336; 1MAH.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004759; F:serine esterase activity; IEA.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000379; Ser_estr.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Signal.
FT SIGNAL
FT CHAIN 19 566
SQ SEQUENCE 566 AA; 62510 MW; 808040F1A407297 CRC64;

Query Match 41.2%; Score 1282; DB 6; Length 566;
Best Local Similarity 45.3%; Pred. No. 2.8e-100;
Matches 251; Conservative 116; Mismatches 177; Indels 10; Gaps 8;

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QY 36 LMACTALGALHTKBPQV-TKYCTLOGQMHV-GKT-PQVGLGVFSPSPPLGILRRPAP 92  
 Db 11 LALFTAWG--HPSPPPVVDVHGKVLGKGVLSSEGTQPVAVFGLGIPFAKPPGRLRFTFP 68  
 QY 93 EPPEPMKIRDATYPPGCLQES-WGQLASMYSTRERYKWLRFSDCLYLNVYAPARAP 151  
 Db 69 QPAEPKSFVNATSYPPMCSQDAVAGVLSLFTNRKENTPLKLSLSDCLYLNIYTPADLT 128  
 QY 152 GDPQLPVMWVPGGATVGAASYESDGLAAREKVVLFLOHRLGIFGLSTDDSHARGN 211  
 Db 129 KQRLPVMWVHGGGLVGAASYDGLAALAHENVVVVIQVRLGFWGFFSTGDEHSRGN 188  
 QY 212 WGLDDMAALRWQENIAAFGGDPGNVTLFGQAGAMSISGLMMSPLASGLFHRALISQSG 271  
 Db 189 WGHLDQLAALRWQDNIAAFGGDPGNVTLFGQAGAMSISGLMMSPLASGLFHRALISQSG 248  
 QY 272 TALFRFITSNPLK-VAKKVAHLAGCNHNSTOILVNCRLALSGTKVMVSNKORFLOLNF 330  
 Db 249 VALTAVLVKKGDKVPLAEQIAAAGCQTITTSAMVHCLRQKTEELLETLLKMKFFSLDL 308  
 QY 331 QRPDEEIIWMSMSPVWDGWIPTDPLVLLTQGVSSVPIYLLGVNLFENLPLVIMKFPPLN 390  
 Db 309 HGDPDRSHPLGTVIDGLLPKTPBELQARKEKNTVPYVWGNKQEFQWIIIPMLKGYPLS 368  
 QY 391 RQAMRKETITKMLWSTRTLNITKEQVPLVVEYLDVNVNHEHDMKMLRNRMMDIVQDATFV 450  
 Db 369 EGKLDQKATMSLLWKSYPVYIAKELIPBATEKYLGGTDPPVKK--KDRFLDALLADVMFS 426  
 QY 451 YATLOAHVHRDAGLVPVLYEFHH-ARGIIVKPRTDGADHGDGMYFLFGGSPATGLSMG 509  
 Db 427 VPSVVARHHRDAGVPTMYEFOYRFSFSDMKPKTVIGDHGDELFSVFGAPFLKEGASE 486  
 QY 510 KEKALSQMKYWANFARTGNPNNDGNLPCWPRYNKDEKYLQDFTTRVGMKLEKXMAFV 569  
 Db 487 BEIRLSQMKYWANFARNNGNPNNGEGLPRWPEYNQEGYLIQIGANTQAAQKLEKXMAFV 546  
 QY 570 MSLYQSORPEKQKQ 583  
 Db 547 TTLFAKKAVERKPPQ 560

## RESULT 6

Q96E58 PRELIMINARY; PRT; 566 AA.  
 ID Q96E58  
 AC Q96E58  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Strausberg R;  
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL; BC012418; AAH12418.1;  
 DR GO; GO:0016787; F:Hydrolase activity; IEA.  
 DR InterPro; IPR002018; CarbesteraseB.  
 DR InterPro; IPR000379; Ser esters.  
 DR Pfam; PF00135; Coesterase\_1.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hypothetical protein; Hydrolase.  
 SQ SEQUENCE 566 AA; 62269 MW; 3B86CBA1C42BAA0F CRC64;

Query Match 40.6%; Score 1265; DB 4; Length 566;  
 Best Local Similarity 43.2%; Pred. No. 7.9e-99;  
 Matches 252; Conservative 111; Mismatches 189; Indels 32; Gaps 8;

QY 6 LPSTVLSLLPTAGAGSMEMWILCWSLITCLMAQTALGALHTKBPQV-TKYCTLOGK-- 62  
 Db 3 LPAULVATL--ASAANG-----HPSPPPVVDVHGKVLGKGV 38  
 QY 63 QMHVGKTIQVFLGVFSPRPPLGILREPAPEPEPMKIRDATYPPGCLQES-SWGLQAS 121  
 Db 39 SLEGPAQVAIFLGIPPAKPPGLRFTPPQPAEPMSFVNATSYPPMCTQDPEKAGQLS 98  
 QY 122 MYVSTRERYKWLRFSEDCLYLVYAPARAGDQPLPVMWVPGGATVGAASYESDGLA 191  
 Db 99 ELFNTRKENIPLKLSLSDCLYLNIYTPADLTQKRLPVMWVHGGGLVGAASYDGLALA 158  
 QY 182 AREKWLIVFQHRIGIFGLSTDDSHARGNWLGLDDMAALRWQENIAAFGGDPGNVTLF 241  
 Db 159 AHENVVVVVIQVRLGFWGFFSTGDEHSRGNWGHLDQVAAALRWQDNIAAFSGNPGSVTIF 218  
 QY 242 GQAGAMSISGLMMSPLASGLFHRALISQSGTALFRFITSNPLK-VAKKVAHLAGCNHNS 300  
 Db 219 GESAGGESVSVLSPKAKLFRALISQSGVALTSVLVKKGDKVPLAEQIAITAGCKTTT 278  
 QY 301 TOILVNCRLALSGTKVMVSNKMRFLQNFQRPDEEIIWMSMSPVWDGWIPTDPLVLLTQ 360  
 Db 279 SAVNVHCLRQKTEELLETLLKMKFFSLDLOGDPRESQPLGTVIDGMLLKTPELQAE 338  
 QY 361 GKVSVPYLLGVNLFENLPLVIMKFPPLNRQAMRKETITKMLWSTRTLNITKEQVPLV 420  
 Db 339 RNHTVPMVGVINKQEFGLPMLMSYPLSEGQDKTAMSLWKSYPVYIAKELIPEA 398  
 QY 421 VEEIIVDNVNEHDMKMLRNRMMDIVQDATFVYATLOAHVHRDAGLVPVLYEFHH-ARGI 479  
 Db 399 TEKILGTD--DTVKKLDLFDLIADVMFGVPSVIVARNHRDAGAPTYMEFOYRFSFSS 456  
 QY 480 IVKPRTDGADHGDGMYFLFGGSPATGLSMGKELASLQMKYWANFARTGNPNNDGNLPCW 539  
 Db 457 DMKPKTVIGDHGDELFSVFGAPFLKEGASEBEIRLSQMKYWANFARNNGNPNNGEGLPHW 516  
 QY 540 PRYNKDEKYLQDFTTRVGMKLEKXMAFMSLYQSORPEKQKQ 583  
 Db 517 PEYNQKEGYLIQIGANTQAAQKLEKXMAFMSLYQSORPEKQKQ 560

## RESULT 7

Q8TD29 PRELIMINARY; PRT; 565 AA.  
 ID Q8TD29  
 AC Q8TD29  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Brain carboxylesterase hBr2.  
 GN CES HBR2.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Hosokawa M., Mori M., Ogasawara Y., Komori C., Tsukada E., Chiba K.;  
 RT "cDNA cloning and expression of carboxylesterase isozymes from human brain."  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Mori M., Hosokawa M., Tsukada E., Ogasawara Y., Chiba K.;  
 RT "cDNA cloning and stable expression of human brain carboxylesterase isozymes."  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL; AB025027; BAB85656.1;  
 DR GO; GO:0016787; F:Hydrolase activity; IEA.  
 DR InterPro; IPR002018; CarbesteraseB.

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CC -1- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL: AF036930; AAC39258.1; -.
DR PDB: 1K4Y; 01-MAY-02.
DR GO: GO:0016787; F:Hydrolase activity; IEA.
DR GO: GO:0004759; F:serine esterase activity; IEA.
DR InterPro: IPR002018; CarbesteraseB.
DR InterPro: IPR000379; Ser esters.
DR Pfam: PFA0135; Coesterase_1.
DR PROSITE: PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE: PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 565 AA; 62291 MW; 0ACD61400CC81D2F CRC64;

Query Match 40.5%; Score 1260; DB 6; Length 565;
Best Local Similarity 43.8%; Pred. No. 2,1e-98;
Matches 245; Conservative 119; Mismatches 180; Indels 16; Gaps 19

Qy 34 LCLMAQTALGAL- ---HTKRPQVY-TKYGLTQKQ--QKHVGKTPIQVLPVFPSPPLGI 86
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 3 LCALLALASLAAC TANGHSPAPVVDTVHGKLVGFVSLGEGFAQPVAVLPVGFPAKPPGLS 62
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 87 LRFAPPPPPPEWKIR DATTVPCCLOE--SWGOLASMYVSTRERYKWLRESEDCLYNV 144
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 63 LRFAPPPQASVSHWKNTSTPFWCSDQAVSGHMLSELTWRKENIP-LKSEDCLYNI 121
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 145 YAPARAPGDPOLPVMVWFPFGAFIVGAASSYEGSDLAAREKVLVFLQHRIGIFGLSTD 204
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 YTPADLTGRGRLPVMVWTHGGGLVMVGASTYDGLALSAHENVVVTIQYRLGIMGFFSTG 181
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 205 DSHARGHWGLLDQMAALRWQENTAAFGGDPGNVTLFQSGAGAMISGLMYKSPLASGLFH 264
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 182 DEHSRGNGWGLDQVAALRWQDNNTANFGGDPGSVTIFGESAGGOSVSLLSPLTKNLPH 241
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 265 RAISQSGTALPRLFTSNPLKVAKKVAHLACNNHSTOILVNCRLRALSQTKVMRVSNKMR 324
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 242 RAISESGVALLSFLFRKTKSLAEKIAEACCKTTTSAMVHCLRQKEEBELMEVTLKWK 301
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 325 FLQNFORDPEELIWSVVDGVVDPDPLVLITQGVKSSVPYLLGVNNLEFNWLLP-Y 383
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 302 FMALDLVGDPKRENTAFITTVIDGVLPRKAPAEILAEKYNMLPYMVGINQOQEFGWII 361
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 384 IMKEPLNQRQMKETITKMLKASTRLTNIITKEQVPLVVEEYLDNVNEHDKMLRNWMDI 443
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 MGLGPLSEGKUDQKATATELLWKSPIVNVSKELTPVATEKYLGGTDDPVKK--KDLFLDM 419
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 444 VQDATFVYATLQTAHYHRDAGLPVLYXFEFH--ARGIIVKPRTPDGADHDEMYFLPGGPF 502
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 420 LADLLFGVPSNVVARRHRDAGAPTYMEYRYRPSFSDMRPKTVIGDGHDEIFSVLGAFF 479
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 503 ATGISMGKEKALSQMKYKWFANFARTGNPDGNLPCWPRYKNKDEKYLQDFTTRVGMKLU 562
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 480 LKEGATEEEIKLSKKWKYKWFANFARNGNPNGEUGPQWPAYDYKSGYLQIGATTQAAQKLU 539
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 563 EKKWAFWMSLY--QSQRPEK 580
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 540 DKEVAFWTELWAKEAPRE 559
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
ID Q9R135 PRELIMINARY; PRT; 565 AA.
AC Q9R135;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Carboxylesterase (EC 3.1.1.1) (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN=Sprague-Dawley;

```



RA Ryu J.W., Lee W., Jung C.Y.;  
 RT "Rattus norvegicus adipocyte carboxylesterase mRNA";  
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL; AF171640; AAD49369.1; -.  
 DR PIR; A45140; A45140.  
 DR HSSP; P21836; IMAA.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004759; F:serine esterase activity; IEA.  
 DR InterPro; IPR0002018; CarbesteraseB.  
 DR Pfam; PF00135; Coesterase; 1.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hydrolase.  
 FT NON TER  
 SQ SEQUENCE 565 AA; 62130 MW; FDDBL9F2C5DD4ECO CRC64;  
 Query Match 40.3%; Score 1254; DB 11; Length 565;  
 Best Local Similarity 42.8%; Pred. No. 6.8e-98;  
 Matches 240; Conservative 120; Mismatches 183; Indels 18; Gaps 6;  
 QY 28 LCWSLTCLMAQTALG-----ALHTKRPQVTVKTYGTLOGKQMVHVKTIQVFLGVPFPR 81  
 DB 6 LWV---LFLAATAWGPSPPPVNTVKGVLGKYNLEGAQ-----PVAVFLGIPFAK 57  
 QY 82 PPLGILFAPPEPEPPKGIKRDATTTPPGCLQES-WGQLASMTVSTRERYKWLRFSEDC 140  
 DB 58 PPLGSLRFAPQPAEPNFKNTTSYPPMCSQDVGQVLSLFTNRKENIPLQFSEDC 117  
 QY 141 YLNYAPARAPGDPQLPVMWFFGGAFIVGAASYEGSDLAAREKVVLPQHLRIGIF 200  
 DB 118 YLNYTTPADLTQKSLRFVWMIHGGVLVGGASTYDQVLSAHENVVVVTIQYRLG 177  
 QY 201 LSTDDSHARGNWGLDQMAALRWQENIAAFGGDPGNVTLFGOSAGMSISGLMWSPLAS 260  
 DB 178 FSTGDESRNGWHLDOVAALHWQDNIANFGNPGSVTIFGESAGFSVALVSLAK 237  
 QY 261 GLFHRAISQSGTALFRFLITSNPLKVAKVHAHAGCNHNSITQLVNCRLALSCTKVM 320  
 DB 238 NLFHRAISESGVLTSAITTSKPIANLIATLSGCKTTTSAVMVHCLRQKTEDELETS 297  
 QY 321 NKRFQLNFORPBEILINSMSPVWGVIPDDPLVLTQGVKSSVPYLLGVNLEFNWL 380  
 DB 298 LKLNLFKDLGLGPKESYFPLPTVIDGVLPKTPPEILAEKSFNTVPYIVGINKQEF 357  
 QY 381 LPYIMKPLNRQARKEKTSITKMLWSTRTLLNITKEQVPLVVEYLDNVNHEHDKMLNR 440  
 DB 358 IPTLMGVPLSEGKLDQKTSKLLKSYPTLKISEKMPVVAEKYFGTD--DPAXRKDL 415  
 QY 441 MDIVQDATFYATLOTAHVHRDAGLPVLYVEFEHARGI-IVKPRTDGADHDEMFL 499  
 DB 416 QDLVADVYFVGVPSVMSRSRHDAGAPTFYFEYRPSFVSAMRPKTVIGDHGDEL 475  
 QY 500 GPATGLSMGKEKALSQMKYWANFARTGNPDGNLPCWPRYNKDEKYLQDLDFTRV 559  
 DB 476 SPFLKDGASEETNLSKVMKYWANFARNGNPNGGGLPHWPEYDQEGYKLGASTQ 535  
 QY 560 KLKEKQAFWMSLYQSOREK 580  
 DB 536 RLKDKVAFWSELRAKEAAEE 556

RESULT 10

O91Y2 ID Q91Y2 PRELIMINARY; PRT; 565 AA.  
 AC Q91Y2;  
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Carboxylic ester hydrolase (EC 3.1.1.1).  
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RN NCBI\_taxid=10116;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Lung;  
 RX MEDLINE=21413896; PubMed=11429416;  
 RA Wallace T.J., Kodis E.M., Langston T.B., Grogan W.M.;  
 RT "Mutation of Residues 423 (Met/Ile), 444 (Thr/Met), and 506 (Asn/Ser)  
 RT Confer Cholesteryl Esterase Activity on Rat Lung Carboxylesterase.";  
 RT SER-506 IS REQUIRED FOR ACTIVATION BY CAMP-DEPENDENT PROTEIN KINASE.";  
 RL J. Biol. Chem. 276:33165-33174 (2001).  
 CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.  
 DR EMBL; L81144; AAL00849.1; -.  
 DR PIR; A45140; A45140.  
 DR GO; GO:0016787; F:hydrolase activity; IEA.  
 DR GO; GO:0004759; F:serine esterase activity; IEA.  
 DR InterPro; IPR0002018; CarbesteraseB.  
 DR Pfam; PF00135; Coesterase; 1.  
 DR PROSITE; PS00122; CARBOXYLESTERASE\_B\_1; 1.  
 DR PROSITE; PS00941; CARBOXYLESTERASE\_B\_2; 1.  
 KW Hydrolase.  
 SQ SEQUENCE 565 AA; 62117 MW; F3294B66AD2141BD CRC64;  
 Query Match 40.2%; Score 1252; DB 11; Length 565;  
 Best Local Similarity 42.8%; Pred. No. 1e-97;  
 Matches 240; Conservative 119; Mismatches 184; Indels 18; Gaps 6;  
 QY 28 LCWSLTCLMAQTALG-----ALHTKRPQVTVKTYGTLOGKQMVHVKTIQVFLGVPFPR 81  
 DB 6 LWV---LFLAATAWGPSPPPVNTVKGVLGKYNLEGAQ-----PVAVFLGIPFAK 57  
 QY 82 PPLGILFAPPEPEPPKGIKRDATTTPPGCLQES-WGQLASMTVSTRERYKWLRFSEDC 140  
 DB 58 PPLGSLRFAPQPAEPNFKNTTSYPPMCSQDVGQVLSLFTNRKENIPLQFSEDC 117  
 QY 141 YLNYAPARAPGDPQLPVMWFFGGAFIVGAASYEGSDLAAREKVVLPQHLRIGIF 200  
 DB 118 YLNYTTPADLTQKSLRFVWMIHGGVLVGGASTYDQVLSAHENVVVVTIQYRLG 177  
 QY 201 LSTDDSHARGNWGLDQMAALRWQENIAAFGGDPGNVTLFGOSAGMSISGLMWSPLAS 260  
 DB 178 FSTGDESRNGWHLDOVAALHWQDNIANFGNPGSVTIFGESAGFSVALVSLAK 237  
 QY 261 GLFHRAISQSGTALFRFLITSNPLKVAKVHAHAGCNHNSITQLVNCRLALSCTKVM 320  
 DB 238 NLFHRAISESGVLTSAITTSKPIANLIATLSGCKTTTSAVMVHCLRQKTEDELETS 297  
 QY 321 NKRFQLNFORPBEILINSMSPVWGVIPDDPLVLTQGVKSSVPYLLGVNLEFNWL 380  
 DB 298 LKLNLFKDLGLGPKESYFPLPTVIDGVLPKTPPEILAEKSFNTVPYIVGINKQEF 357  
 QY 381 LPYIMKPLNRQARKEKTSITKMLWSTRTLLNITKEQVPLVVEYLDNVNHEHDKMLNR 440  
 DB 358 IPTLMGVPLSEGKLDQKTSKLLKSYPTLKISEKMPVVAEKYFGTD--DPAXRKDL 415  
 QY 441 MDIVQDATFYATLOTAHVHRDAGLPVLYVEFEHARGI-IVKPRTDGADHDEMFL 499  
 DB 416 QDLVADVYFVGVPSVMSRSRHDAGAPTFYFEYRPSFVSAMRPKTVIGDHGDEL 475  
 QY 500 GPATGLSMGKEKALSQMKYWANFARTGNPDGNLPCWPRYNKDEKYLQDLDFTRV 559  
 DB 476 SPFLKDGASEETNLSKVMKYWANFARNGNPNGGGLPHWPEYDQEGYKLGASTQ 535  
 QY 560 KLKEKQAFWMSLYQSOREK 580  
 DB 536 RLKDKVAFWSELRAKEAAEE 556

RESULT 11

O9UK7 ID Q9UK77 PRELIMINARY; PRT; 567 AA.

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AC Q9UK77;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Egsyn.
OC Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Islam M.R., Waheed A., Shah G.N., Tomatsu S., Sly W.S.:
RT "Human Egsyn Binds beta-Glucuronidase But Neither the Esterase Active
RT Site of Egsyn Nor the C Terminus of beta-Glucuronidase Is Involved in
RT Their Interaction.";
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AF177775; AD53175.1; -.
DR HSP; P21836; IWAH.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR002018; CarbesteraseB.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase.
SQ SEQUENCE 567 AA; 62448 MW; CC445067DC79BC59 CRC64;

Query Match 40.1%; Score 1248.5; DB 4; Length 567;
Best Local Similarity 44.7%; Pred. No. 2e-97;
Matches 248; Conservative 109; Mismatches 187; Indels 11; Gaps 8;

QY 36 LMAQTALGALHTKRPQV--TKYGTLOGK--QMHVGTPIQVFLGVSPSPGILRFPAP 92
DB 11 LSAAAWG--HPSSPPVVDVTHGKVLGVSLSGFAQPAIFLIGIFPAKPLGLRFTTP 68

QY 93 EPPEPWKGIKRDATYPPGCLQE--SWGQLASMYVSTRERYKWLRFSDCLYLYNYPARAP 151
DB 69 QPAPSPVKNATSPYPMCTQDPKAGQLLSELFTNRKENIPKLSEDCLYLYNYPADLT 128

QY 152 GDPQLPVMWFFPGAFIVGAASSYEGSDLAAREKVLVFLQHLRIGLFGFLSTDDSHRGN 211
DB 129 KQRLPVMWTHGGGLVGAASVYDGLAALAHENVVVVTIYQRLGIVGWFFSTGDSHSGN 188

QY 212 WGLDDQALRWQENIAAAGDPPGNVTLFGQAGAMSISGLMWSPLASGLPHRAISQSG 271
DB 189 WGHLDQVAALRWQDNIAAGDPPGNVTLFGQAGAMSISGLMWSPLASGLPHRAISQSG 248

QY 272 TALFRLFTSNPLK--VAKKVAHLACGNHNSQIILVNCRLALSGTKVMRNSKVRFLQNLN 330
DB 249 VALTSVLVKGDDVPLAEQIAITAGCKTTTSAVMVHCLRQKTEBEELETTLKMKFLSLDL 308

QY 331 QRDPEEIIWMSPVVDGVVPPDDPLVLLTQGVSSVYPYLLGVNVLNLEFNLPL--YIMKFLP 389
DB 309 QGDPRSOPFLGTVIDGMLLTKTEELQAEENFTVPMVGINQKQEFGLNIPQLMSYPL 368

QY 390 NRQAMRETIITKMLWSTRTLINITKEQVPLVVEEYLDNVNHDWMLRMMDIVODATF 449
DB 369 SEGQLDQKNTANSLWKSVPYLCIAKELIPEATEKYLGGTD--DVTXKKDLFLDLIAVDF 426

QY 450 VYATLQTAHYRDRDAGLPVLYEPEHH--ARGLIVKPRTDGADHGDMDYFLFGGPAFLGSM 508
DB 427 GVPSPVIVARNRDAGAPTYMEFYQRPFSFSDMKPKTVIGDHGDELFSVFGAPFLKEGAS 486

QY 509 GKERALSQMKYKWPANPARTCNPDGNLPCWPRYNKDEKYLQLDFTTRVGKMLKEKNQAF 568
DB 487 EEEIRLSQMKYKWPANPARTCNPDGNLPCWPRYNKDEKYLQLDFTTRVGKMLKEKNQAF 546

QY 569 WWSLYSQORPEKQKQ 583
DB 547 WTNLFAKKAVEKPPQ 561
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RESULT 12
C35534
ID O35534 PRELIMINARY; PRT; 565 AA.
AC O35534;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Carboxylesterase precursor (EC 3.1.1.1).
GN CARBOXYLESTERASE.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Syrian golden; TISSUE=Liver;
RA Sone T., Ishida Y., Takabatake E., Wang C., Isobe M.;
RT "Cloning and expression of a hamster liver cDNA encoding a novel
RT carboxylesterase which catalyzes the activation of carcinogenic
RT arylhydroxamic acids.";
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; D50578; BAA23604.1; -.
DR HSP; P21836; IWAH.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004759; F:serine esterase activity; IEA.
DR InterPro; IPR002018; CarbesteraseB.
DR Pfam; PF00135; Coesterase; 1.
DR PROSITE; PS00122; CARBOXYLESTERASE_B_1; 1.
DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
KW Hydrolase; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT CHAIN 19 565 CARBOXYLESTERASE.
SQ SEQUENCE 565 AA; 62188 MW; 8273233A59DFIED0 CRC64;

Query Match 40.1%; Score 1247; DB 11; Length 565;
Best Local Similarity 42.7%; Pred. No. 2.7e-97;
Matches 240; Conservative 119; Mismatches 189; Indels 14; Gaps 8;

QY 26 WT--LCWLSLTCLMAQTALGALHTKRPQV--TKYGTLOGKQMHVG--KTPQVFLGVSPFS 80
DB 2 WLYPLVW---ISLAACATAG--HPSSPPVVDVTHGKVLGVSLSGFAQPAIFLIGIFPA 56

QY 81 RPPLGILRFAPEPPPEPWKGIKRDATYPPGCLQES--WGQLASMYVSTRERYKWLRFSDC 139
DB 57 KPPLGSLRFAPEPPPEPWKGIKRDATYPPGCLQES--WGQLASMYVSTRERYKWLRFSDC 116

QY 140 LYLNYVYAPARAPGDPQLPVMWFFPGAFIVGAASSYEGSDLAAREKVLVFLQHLRIGLFG 199
DB 117 LYLNTYTPADLTNKSRLPVMWTHGGGLVGAASVYDGLAALAHENVVVVTIYQRLGIVG 176

QY 200 FLSTDDSHARGNWGLDDQALRWQENIAAAGDPPGNVTLFGQAGAMSISGLMWSPLA 259
DB 177 FSTGDSHARGNWGLDDQALRWQENIAAAGDPPGNVTLFGQAGAMSISGLMWSPLA 236

QY 260 SGLFHRAISQSGTALFRLFTSNPLKVAHLACGNHNSQIILVNCRLALSGTKVMRNV 319
DB 237 KNLFHRAISQSGTALFRLFTSNPLKVAHLACGNHNSQIILVNCRLALSGTKVMRNV 296

QY 320 SNMKRFLQNLNFORDEEIIWMSPVVDGVVPPDDPLVLLTQGVSSVYPYLLGVNVLNLEF 379
DB 297 SQMNLFLKLDLGNPKRETYPPFLPTWIDGVFLSKSEEEILAEKSFNTVPMVGINQKQEG 356

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QY 440 MMDIVODATFVYATLQTAHYRDRDAGLPVLYEPEHH--ARGLIVKPRTDGADHGDMDYFL 498
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RESULT 15

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ID Q924V8 PRELIMINARY; PRT; 565 AA.
AC Q924V8;
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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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GN CES3 OR CESMMH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J, TISSUE=Liver;
RA Hosokawa M., Nakamura T., Nakata F., Takahashi D., Sakae M., Satoh T.,
RA Chiba K.;
RT "Purification, molecular cloning and expression of cDNA encoding
RT peroxisome proliferator inducible carboxylesterase isozymes from
RT C57BL/6 mouse liver."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TYPE-B CARBOXYLESTERASE/LIPASE FAMILY.
DR EMBL; AB023631; BAB60598.1; -.
DR MGD; MGI:2148202; Ces3.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004759; F:serine esterase activity; IEA.
DR InterPro; IPR002018; CarbesteraseB.
DR InterPro; IPR000379; Ser_estis.
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DR PROSITE; PS00941; CARBOXYLESTERASE_B_2; 1.
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 11, 2004, 09:15:47 ; Search time 6837.73 Seconds  
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Title: US-10-001-227-3

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Scoring table: IDENTITY\_NUC  
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Searched: 3470272 seqs, 21671516995 residues  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	1752	100.0	1983	6	AX469746	AX469746	Sequence
3	1752	100.0	2081	6	AX377796	AX377796	Sequence
4	1356.4	77.4	2178	6	AX833215	AX833215	Sequence
5	1356.4	77.4	2178	9	AK094783	AK094783	Homo sapi
6	1059	60.4	2448	10	BC026374	BC026374	Mus muscu
7	957.18	54.7	2456	6	AX375990	AX375990	Sequence
8	957.18	54.7	2456	6	AX469751	AX469751	Sequence
9	957.18	54.7	2456	9	AX358504	AX358504	Homo sapi
10	902	51.5	2178	6	AX377795	AX377795	Sequence
11	601.6	34.3	1602	6	AX921060	AX921060	Sequence
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13	431.8	24.6	1923	4	AB023629	AB023629	Canis fam
14	428.8	24.5	1717	4	AF036930	AF036930	Cryptolog
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## ALIGNMENTS

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DEFINITION	Sequence 3 from Patent WO244357.
ACCESSION	AX469748
VERSION	AX469748.1 GI:21901870
KEYWORDS	.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1
REFERENCE	Kapeller-Libermann,R. and Silos-Santiago,I. Methods of using 18903 to treat pain and pain-related disorders Patent: WO 0244357-A 3 06-JUN-2002;
AUTHORS	JOURNAL
TITLE	PATENT
ABSTRACT	





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Db 1741 CAGAGCAATC 1752

RESULT 2
AX469746
LOCUS AX469746 1983 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 1 from Patent WO244357.
ACCESSION AX469746
VERSION AX469746.1 GI:21901868
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE
Kapeller-Libermann,R. and Silos-Santiago,I.
TITLE Methods of using 18903 to treat pain and pain-related disorders
JOURNAL Patent: WO 0244357-A 1 06-JUN-2002;
Millennium Pharmaceuticals, Inc. (US)
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Location/Qualifiers
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RESULT 3
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LOCUS AX377796 2081 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 29 from Patent WO0212467.
ACCESSION AX377796
VERSION AX377796.1 GI:19573887
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Baughn,M.R., Bruns,C.M., Das,D., Deleage,A.M., Ding,L.,
Elliot,V.S., Gandhi,A.R., Griffin,J.A., Hafalia,A.J., Khan,F.A.,
Lal,P., Lee,S., Lu,D.A., Lu,Y., Patterson,C., Ramkumar,J.,
Ring,H.Z., Sanjanwala,M.S., Tang,Y.T., Thornton,M. and
Tribouley,C.M.
TITLE Drug metabolizing enzymes
JOURNAL Patent: WO 0212467-A 29 14-FEB-2002;
Incyte Genomics, Inc. (US)
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DEFINITION Sequence 339 from Patent EP1347046.  
ACCESSION AX833215  
VERSION AX833215.1 GI:39919350  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Isogai, T., Sugiyama, T., Otsuki, T., Wakamatsu, A., Sato, H., Ishii, S., Yamamoto, J. I., Isono, Y., Hio, Y., Otsuka, K., Nagai, K., Irie, R., Tamechika, I., Seki, N., Yoshikawa, T., Otsuka, M., Nagahari, K. and Masuho, Y.  
TITLE Full-length cDNA sequences  
JOURNAL Patent: EP 1347046-A 339 24-SEP-2003;  
Research Association for Biotechnology (JRP)  
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## RESULT 6

LOCUS BC026374 2448 bp mRNA linear ROD 06-OCT-2003  
DEFINITION Mus musculus cDNA sequence BC026374, mRNA (cDNA clone MGC:31116  
IMAGE:4163362), complete cds.

ACCESSION BC026374.1 GI:20071335

VERSION BC026374.1

KEYWORDS MGC.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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1 (bases 1 to 2448)

Srausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.

Klausner, R.D., Collins, F.S., Wegner, L., Shemen, C.W., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullaly, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Buffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.B.,

Scherer, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL 2388257

MEDLINE 12477932

PUBMED 2 (bases 1 to 2448)

REFERENCE Srausberg, R.

TITLE  
JOURNALREMARK  
COMMENT

Direct Submission  
Submitted (02-APR-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shec.stanford.edu>  
Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 43 Row: c Column: 24  
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LOCUS	AX375990	2456 bp	DNA linear PAT 01-MAR-2002
DEFINITION	Sequence 57 from Patent WO0168848.		
ACCESSION	AX375990		
VERSION	AX375990.1 GI:19170388		
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	Baker,K.P., Chen,J., Desnoyers,L., Goddard,A., Godowski,P.J.,		
	Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and		
	Zhang,Z.		
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding		
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JOURNAL	Patent: WO 0168848-A 57 20-SEP-2001,		
	Genentech, Inc. (US)		
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Qy	187	CAGATGATGTGGGAAGACACCCATCCAAGTCTTTTAGAGTCCCTTCTCCAGACCT	246
Db	448	CAGATGATGTGGGAAGACACCCATCCAAGTCTTTTAGAGTCCCTTCTCCAGACCT	507



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QY 307 GATGCTACCACTACCGGCTG-----328
Db 568 GATGCTACCACTACCGGCTGATGGAGTCTCGCTCTGTGCGCAGGCTGGAGTGCAGTG 527
QY 329 -----328
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LOCUS AX469751 2456 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 6 from Patent WO0244357.
ACCESSION AX469751
VERSION AX469751.1 GI:21901872
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Kapeller-Libermann, R. and Silos-Santiago, I.
AUTHORS Methods of using 18903 to treat pain and pain-related disorders
TITLE Patent: WO 0244357-A 6 06-JUN-2002;
JOURNAL Millennium Pharmaceuticals, Inc. (US)
FEATURES
Location/Qualifiers
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ORIGIN
Query Match 54.7%; Score 957.8; DB 6; Length 2456;
Best Local Similarity 85.3%; Pred. No. 3.7e-195; Indels 201; Gaps 2;
Matches 1180; Conservative 0; Mismatches 2;

QY 127 GGTGCTTTCACACCAAGAGGCTCAAGTGTGTACCAAAATATGGAACCTTCAAGGAAA 186
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LOCUS AX377795 2178 bp DNA linear PAT 18-MAR-2002  
DEFINITION Sequence 28 from Patent WO212467.  
ACCESSION AX377795  
VERSION AX377795.1 GI:19573886  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS Baughn, M.R., Bruns, C.M., Das, D., Deleage, A.M., Ding, L.,  
Elliot, V.S., Gandhi, A.R., Griffin, J.A., Hafalia, A.J., Khan, F.A.,  
Lai, P., Lee, S., Lu, D.A., Lu, Y., Patterson, C., Ramkumar, J.,  
Ring, H.Z., Sanjanwalla, M.S., Tang, Y.T., Thornton, M. and  
Tribouley, C.M.  
TITLE Drug metabolizing enzymes  
JOURNAL Patent: WO 0212467-A 28 14-FEB-2002;  
Incyte Genomics, Inc. (US)  
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**LOCUS**  
**DEFINITION** Felis catus CBS1 mRNA for carboxylesterase, complete cds.  
**ACCESSION** AB094147  
**VERSION** AB094147.1 GI:30038512  
**KEYWORDS**  
**SOURCE** Felis catus (cat)  
**ORGANISM** Felis catus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
**REFERENCE**  
**AUTHORS** Miyazaki, M., Sai, H., Taira, H. and Yamashita, T.  
**TITLE** Molecular cloning of the feline liver carboxylesterase  
**JOURNAL** unpublished  
**REFERENCE** 2 (bases 1 to 1985)  
**AUTHORS** Miyazaki, M., Sai, H., Taira, H. and Yamashita, T.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (19-OCT-2002) Masao Miyazaki, Iwate University,  
 Department of Agro-bioscience, Faculty of Agriculture, 3-18-8 Ueda,  
 Morioka, Iwate 020-8550, Japan (E-mail: cdg#3700@par.odn.ne.jp,  
 Tel: 81-19-621-6157, Fax: 81-19-621-6177)  
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RESULT 13

AB023629

LOCUS AB023629 1923 bp mRNA linear MAM 09-JUN-2001

DEFINITION Canis familiaris CBSdb1 mRNA for carboxylesterase D1, complete cds.

ACCESSION AB023629

VERSION AB023629.1 GI:14331124

KEYWORDS carboxylesterase D1; Dog liver carboxylesterase D1.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (sites)

AUTHORS Hosokawa,M., Suzuki,K., Takahashi,D., Mori,M., Satoh,T. and Chiba,K.

TITLE Purification, molecular cloning, and functional expression of dog liver microsomal acyl-CoA hydrolase: a member of the carboxylesterase multigene family

Arch. Biochem. Biophys. 389 (2), 245-253 (2001)

21237951

JOURNAL MEDLINE

PUBMED 11339814

REFERENCE 2 (bases 1 to 1923)

AUTHORS Hosokawa,M.

TITLE Direct Submission

JOURNAL Submitted (11-FEB-1999) Masakiyo Hosokawa, Chiba University, Faculty of Pharmaceutical Sciences, 1-33 Yayoi-cho, Chiba, Chiba 263-8522, Japan (E-mail:masakiyo@p.chiba-u.ac.jp, Tel:81-43-290-2921, Fax:81-43-290-2921)

FEATURES

source

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AF036930
VERSION
AF036930.1 GI:3219694
KEYWORDS
Oryctolagus cuniculus (rabbit)
SOURCE
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ORGANISM
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REFERENCE
1 (bases 1 to 1717)
Potter, P.M., Pawlik, C.A., Morton, C.L., Naeve, C.W. and Danks, M.K.
Isolation and partial characterization of a cDNA encoding a rabbit
liver carboxylesterase that activates the prodrug irinotecan
(CPT-11)
Cancer Res. 58 (12), 2646-2651 (1998)
JOURNAL
MEDLINE
98297515
PUBMED
9635592
REFERENCE
2 (bases 1 to 1717)
Potter, P.M.
Direct Submission
Submitted (02-DEC-1997) Molecular Pharmacology, St. Jude Children's
Research Hospital, 332 North Lauderdale, Memphis, TN 38105, USA
JOURNAL
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